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OM protein - protein search, using sw model

Run on: June 21, 2004, 10:18:09 ; Search time 65.5868 Seconds
(without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-6
Perfect score: 5912
Sequence: 1 MATRAVCVLKGGPGVQGIIN.....GNKDRRSTGKSGWKGFGYWP 1099

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5912	100.0	1099	5 AAU76378	Aau76378 HCV multi
2	5912	100.0	1099	6 ABG72262	Abg72262 HCV multi
3	4032	68.2	829	5 AAE18690	Aae18690 Multiple
4	4032	68.2	829	7 ADC06769	Adc06769 Chimeric
5	3829.5	64.8	1021	2 AAU34481	Aaw34481 HCV anti
6	3829.5	64.8	1021	2 AAU40039	Aaw40039 Fusion pr
7	3829.5	64.8	1021	5 AAU22050	Aae22050 pSOD/c200
8	3050.5	51.6	841	2 AAR68547	Aar68547 HCV prote
9	3050.5	51.6	841	6 ABO27020	Abo27020 Hepatitis
10	3050.5	51.6	841	7 ADA07875	Ada07875 HCV prote
11	3047.5	51.5	841	2 AAU01701	Aaw01701 hSOD-HCV
12	3047.5	51.5	841	2 AAU46397	Aaw46397 Amino aci
13	3047.5	51.5	841	2 AAU97609	Aaw97609 Amino aci
14	3042.5	51.5	840	2 AAR14349	Aar14349 HCV prote
15	2909.5	49.2	2261	1 AAP90164	Aap90164 Peptide e
16	2909.5	49.2	2436	1 AAP92050	Aap92050 Sequence
17	2909.5	49.2	2436	1 AAP90288	Aap90288 Peptide e
18	2909.5	49.2	2772	3 AAB18540	Aab18540 Protein e
19	2909.5	49.2	2955	2 AAY14975	Aay14975 Amino aci
20	2909.5	49.2	2955	3 AAR18541	Aar18541 Polypeptide
21	2909.5	49.2	3011	2 AAR90931	Aar90931 Hepatitis
22	2909.5	49.2	3011	2 AAW34480	Aaw34480 HCV polyp
23	2909.5	49.2	3011	2 AAW40038	Aaw40038 HCV polyp
24	2909.5	49.2	3011	2 AAE22049	Aae22049 Hepatitis
25	2906.5	49.2	2301	1 AAP92047	Aap92047 Sequence

ALIGNMENTS

RESULT 1

AAU76378 ID AAU76378 standard; protein; 1099 AA.

XX AC AAU76378;

XX XX 08-MAY-2002 (first entry)

DE DE HCV multiple epitope fusion antigen (MEFA) 7.1 protein sequence.

XX KW Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;
KW immunosay solid support; multiple epitope fusion antigen; MEFA;
KW non-structural protein.

XX OS Hepatitis C virus.

XX OS Synthetic.

PN WO200196870-A2.

XX XX 20-DEC-2001.

XX XX 14-JUN-2001; 2001WO-US019156.

PR 15-JUN-2000; 2000US-0212082P.

PR 02-APR-2001; 2001US-0280811P.

XX XX 02-APR-2001; 2001US-0280867P.

PA (CHIR) CHIRON CORP.

XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
PI Medina-Selby A;

XX WPI; 2002-090228/12.

DR N-PSDE; ABK15345.

XX Immunosay solid support, useful for detecting hepatitis C virus
PT infection in biological sample, comprises HCV NS3/4a conformational
PT epitope and multiple epitope fusion antigen bound to the support.

XX Claim 5; Fig 5; 92pp; English.

XX The present invention relates to a new immunoassay solid support
CC consisting essentially of at least one hepatitis C virus (HCV) NS3/4a
CC conformational epitope and a multiple epitope fusion antigen (MEFA),
CC bound to the support. The NS3/4a conformational epitope and/or MEFA
CC reacts specifically with anti-HCV antibodies present in a biological
CC sample from an HCV-infected individual. The immunoassay of the invention
CC is useful for detecting hepatitis C virus infection in a biological

Aar08123 Hepatitis
Aar21519 Compiled
Aau84597 HCV polyp
Aar25135 HCV polyp
Aap92041 Hepatitis
Aar24440 Composite
Aar34009 HCV-1 pol
Aar31621 Hepatitis
Aap90158 Protein s
Aar70230 Composite
Aar28582 HCV amino
Aar08124 Hepatitis
Aae22052 Hepatitis
Aaw77397 Hepatitis
Aap71460 Amino aci
Aau99289 Hepatitis
Aab61848 HCV H77 c
Aae00442 Hepatitis
Aaw77398 Hepatitis
Aaw98021 Infectiou

26 2906.5 49.2 2772 2 AAR08123
27 2900.5 49.1 3011 2 AAR21519
28 2900.5 49.1 3011 5 AAU84597
29 2897.5 49.0 2435 2 AAR25135
30 2896.5 49.0 1766 1 AAP92041
31 2895.5 49.0 2894 2 AAR24440
32 2893.5 48.9 2816 2 AAR34009
33 2891.5 48.9 3011 2 AAR31621
34 2890.5 48.9 1786 1 AAP90158
35 2890.5 48.9 2894 2 AAR70230
36 2883.5 48.8 2436 2 AAR28582
37 2880.5 48.7 2955 2 AAR08124
38 2877.5 48.7 3011 5 AAE22052
39 2875 48.6 3011 2 AAW77397
40 2875 48.6 3011 6 ABP71460
41 2875 48.6 3012 5 AAU99289
42 2875 48.6 3012 6 ABU61848
43 2868 48.5 2984 4 AAE00442
44 2868 48.5 3011 2 AAW77398
45 2868 48.5 3011 2 AAW98021

KW non-A, non-B hepatitis; NANB; multiple epitope fusion antigen 12; MEFA12;
 KW chimeric.
 XX OS Chimeric.
 OS Synthetic.
 OS Unidentified.
 OS Hepatitis C virus.
 OS Homo sapiens.
 XX US2002192639-A1.
 XX 19-DEC-2002.
 XX 14-JUN-2001; 2001US-00881239.
 XX 15-JUN-2000; 2000US-0212082P.
 PR 02-APR-2001; 2001US-0280811P.
 PR 02-APR-2001; 2001US-0280867P.
 XX (CHIE/) CHIEN D Y.
 PA (ARCA/) ARCANGEL P.
 PA (TAND/) TANDESKE L.
 PA (GEOR/) GEORGE-NASCIMENTO C.
 PA (COIT/) COIT D.
 PA (MEDI/) MEDINA-SELBY A.
 XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
 PI Medina-Selby A;
 PI WPI; 2003-644609/61.
 DR N-PSDB; ADC06770.
 XX
 PT Immunoassay solid support for detecting hepatitis C virus infection in
 PT biological samples, comprises a hepatitis C virus anti-core antibody and
 PT an isolated hepatitis C virus NS3/4a epitope bound HCV anti-core
 PT antibody.
 XX Claim 45; Fig 7; 40pp; English.
 PS
 PS The invention relates to a novel immunoassay solid support comprising at
 CC least one hepatitis C virus (HCV) anti-core antibody and at least one
 CC isolated HCV NS3/4a (non-structural protein 3/4a) epitope bound thereto.
 CC The system of the invention may be useful for detecting HCV infection in
 CC a biological sample and for treating or detecting non-A, non-B hepatitis
 CC (NANB hepatitis). The current sequence is that of the chimeric multiple
 CC epitope fusion antigen 12 (MEFA12) protein of the invention.
 XX
 SQ Sequence 829 AA;
 Query Match 68.2%; Score 4032; DB 7; Length 829;
 Best Local Similarity 69.8%; Pred. No. 2e-275;
 Matches 791; Conservative 1; Mismatches 3; Indels 338; Gaps 7;
 QY 1 MATKAVCLVKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
 DB 1 MATKAVCLVKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
 QY 61 AGPHFNLGRKHGGPKDEERHVGDLGNVTADKGVADVSTEDSVISLSDHCHCIIGRTLTV 120
 DB 61 AGPHFNLSTR----- 71
 QY 121 HEKADDLGKGNNEESTKTGNAGSRLACGVIGIAQNLNSGNCNSIYPGHITGHRMAWKLGS 180
 DB 72 -----GCNCSIYPGHITGHRMAWKLGS 93
 QY 181 AARTTSGFVSLFAPGAKQNEHTVTGAAARTTSLTSLFSPGASQNIQLIVDFIPVENLE 240
 DB 94 AARTTSGFVSLFAPGAKQNEHTVTGAAARTTSLTSLFSPGASQNIQLITS----- 145
 QY 241 TTRSRPFVTDNSPPVPPVPSQFVAHLHAPTGSKSTKVPAAYAAQGVKVLVILNPSVAATL 300
 DB 146 -----TDNSPPVPPVPSQFVAHLHAPTGSKSTKVPAAYAAQGVKVLVILNPSVAATL 197

QY 301 GFGAYNSKAHGIDPNIRTVGRTITTTGSPITTYSTYKFLADGCGSGAYDIIICDECHSTD 360
 DB |||||
 198 GFGAYNSKAHGIDPNIRTVGRTITTTGSPITTYSTYKFLADGCGSGAYDIIICDECHSTD 257
 QY 361 ATSIILGIGTVLDOAETAGARLVVLATATPPGVTTPHNIEBVALSTGEIEFFYKAIPL 420
 DB |||||
 258 ATSIILGIGTVLDOAETAGARLVVLATATPPGVTTPHNIEBVALSTGEIEFFYKAIPL 317
 QY 421 EVIKGRHLIFCHSKKCKDELAALKVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMT 480
 DB |||||
 318 EVIKGRHLIFCHSKKCKDELAALKVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMT 377
 QY 481 GYTGFDSVIDONTCTVTQTFDSLDPTFTIETITLPQDAVSTQRTGRGKPGIYRFV 540
 DB |||||
 378 GYTGFDSVIDCNTC----- 392
 QY 541 APGERPSGMFDSVSLCECYDAGCAWVELTPAETTVRLRAYMNTPGLPVQCDHLEFWEVGF 600
 DB ----- 392
 601 TGLTHIDAHFLSQTKSGENLPYLVAQATVCARQAAPPSPWDQMKCLIRLKTLLHGT 660
 DB ----- 392
 661 PLYRLGAVQNEITLTHPVTKYIMTMSADLEVTTSACSGKPAIIPDREVLIREPDEME 720
 DB |||||
 393 -----ACSGKPAIIPDREVLIREPDEME 416
 QY 721 CSQHLPLYEQGMMLAEQFKALGSRGKPAIIPDKEVLYQYDEMEECSQAAPYIEQA 780
 DB CSQHLPLYEQGMMLAEQFKALGSRGKPAIIPDKEVLYQYDEMEECSQAAPYIEQA 476
 QY 781 QVIAHQFKEKVLGLINDQVVVTPDKEILYEAFDEMEECASKAALIEGQORVAEMLKSKI 840
 DB QVIAHQFKEKVLGLINDQVVVTPDKEILYEAFDEMEECASKAALIEGQORVAEMLKSKI 536
 QY 841 QGLLGLLRRHVGPGEGAVQMMNRLTAFASRGHNHVSPTHYVPSRSRFAQALPVWARP 900
 DB QGLLGLLRRHVGPGEGAVQMMNRLTAFASRGHNHVSPTHYVPSRSRFAQALPVWARP 596
 QY 901 PPLVETWKKPDYEPVPHGSRRRFAQALPVWARPDPNPPLVETWKKPDYEPVPHGRT 960
 DB 597 PPLVETWKKPDYEPVPHGSRRRFAQALPVWARPDPNPPLVETWKKPDYEPVPHGRT 656
 QY 961 KXNTNRRPDQVKFPGGGQIVG-----RRGP-----PIKARPEGRGTWAPGY 1003
 DB KXNTNRRPDQVKFPGGGQIVG|||PRGPRGLGLATRKTSPIKARPEGRGTWAPGY 716
 QY 1004 PWPLYGNKDRRSTGKSWGKPGYVPRKTKNTNRRPDQVKFPGGGQIVG-----RRGP- 1056
 DB 717 PWPLYGNKDRRSTGKSWGKPGYVPRKTKNTNRRPDQVKFPGGGQIVG|||PRRGR 776
 QY 1057 -----PIPKARPEGRGTWAPGYPWPLYGNKDRRSTGKSWGKPGYVPPW 1099
 DB 777 LGVLATRKTSPIPKARPEGRGTWAPGYPWPLYGNKDRRSTGKSWGKPGYVPPW 829
 RESULT 5
 AAW34481
 ID AAW34481 standard; protein; 1021 AA.
 XX
 AC AAW34481;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-MAR-1998 (first entry)
 XX
 DE HCV antigen combination pSOD/c200/core.
 XX
 KW PCR primer; amplify; HCV; hepatitis c virus; antigen combination; NS3;
 KW C domain; S domain; NS5; HCV polypeptide; anti-HCV antibody; detection;
 KW NS4.
 XX
 OS Hepatitis C virus.

OS Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 1..902 /note= "linker"
FT FT
FT Misc-difference 1..154 /note= "hSOD fragment"
FT FT
FT Misc-difference 155..159 /note= "linker"
FT FT
FT Misc-difference 160..899 /note= "c200 (amino acids 1192-1931 of HCV polyprotein)"
FT FT
FT Misc-difference 903..1021 /note= "c22 (amino acids 2-120 of HCV polyprotein)"
XX XX
XX US5683864-A.
XX DD
XX 04-NOV-1997.
XX XX
XX 07-JUL-1992; 92US-00910760.
XX XX
XX 18-NOV-1987; 87US-00122714.
XX PR
XX 30-DEC-1987; 87US-00139886.
XX PR
XX 26-FEB-1988; 88US-00161072.
XX PR
XX 06-MAY-1988; 88US-00191263.
XX PR
XX 26-OCT-1988; 88US-00263584.
XX PR
XX 14-NOV-1988; 88US-00271450.
XX PR
XX 17-MAR-1989; 89US-00325338.
XX PR
XX 20-APR-1989; 89US-00341334.
XX PR
XX 21-APR-1989; 89US-00353896.
XX PR
XX 18-MAY-1989; 89US-00355002.
XX PR
XX 04-APR-1990; 90US-00504352.
XX PR
XX (CHIR) CHIRON CORP.
XX PA
XX Kuo G, Houghton M, Choo Q;
XX WPI; 1997-548976/50.
XX DR
XX N-PSDB; AAT99982.
XX XX
XX Combination of three hepatitis C virus antigens - used for detection of
XX specific antibodies to diagnose infection.
XX
XX Example 6; Col 59-68; 57pp; English.
XX
XX This sequence represents a Hepatitis c virus (HCV) antigen combination of
XX the invention. The HCV antigen combination comprises an antigen (Ag1)
XX comprising the C domain (i.e. amino acids (aa) 1-120 of the HCV
XX polyprotein), or its immunologically reactive fragment containing at
XX least 8 aa. It also comprises two additional antigens from two different
XX polyprotein domains, including at least 8 aa from the NS3, NS4, S or NS5
XX domains of the polyprotein, corresponding, respectively, to aa 1050-1640;
XX 1640-2000; 1200-400 and 2000-3011 of the HCV polyprotein. Alternatively,
XX Ag1 contains at least 8 aa from the 1-122 or 9-177 aa regions of the HCV
XX polyprotein. These antigen combinations are used diagnostically to detect
XX anti-HCV antibodies, using any standard immunoassay format. These antigen
XX combinations have a broader range of reactivity with antibodies than any
XX antigen individually. (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 1021 AA;
SQ
Query Match 64.8%; Score 3829.5; DB 2; Length 1021;
Best local Similarity 67.2%; Pred. No. 5.2e-261;
Matches 784; Conservative 24; Mismatches 79; Indels 279; Gaps 17;
QY 1 MATKAVCVLKGDGVPQGIINFEQKESGPKVWGSIKGLTEGLHGFVHFGDNTAGTS 60
DB 1 MATKAVCVLKGDGVPQGIINFEQKESGPKVWGSIKGLTEGLHGFVHFGDNTAGTS 60
QY 61 AGPHFNPLSRKHGPKDEERHVGDLGNVTADKGDVADVSDIEDSVISLGDHCHIIIGRTLV 120
DB 61 AGPHFNPLSRKHGPKDEERHVGDLGNVTADKGDVADVSDIEDSVISLGDHCHIIIGRTLV 120
QY 121 HEKADDLCKGNEESTKTGNAGSLACGVIGIAQNLEFGA----- 160
XX

RESULT 6

AAW40039
 ID AAW40039 standard; protein; 1021 AA.
 AC AAW40039;
 XX
 DT 26-MAY-1998 (first entry)
 XX
 DE Fusion protein c200/c22.
 XX
 KW Hepatitis C virus C domain; HCV; immunological activity; c200/c22;
 KW NS3 domain; NS4 domain; S domain; NS5 domain; fusion protein.
 XX
 OS Synthetic.
 OS Hepatitis virus.
 XX
 PN US5712087-A.
 XX
 XX 27-JAN-1998.
 XX
 PD 12-MAY-1995; 95US-00440519.
 XX
 PF 04-APR-1990; 90US-00504352.
 XX
 PR 07-JUL-1992; 92US-00910760.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 XX Kuo G, Houghton M, Choo Q;
 PI WPI; 1998-119973/11.
 XX N-PSDB; AAV09990.
 DR
 XX
 PT Immunoassays for hepatitis C virus antibodies - using combinations of
 PT antigenic fragments of HCV polyprotein.
 XX
 PS Example 6; Fig 4; 59pp; English.
 XX
 CC This sequence represents a fusion protein constructed from the hepatitis
 CC C virus core domain (which is situated at the carboxy terminus of the
 CC fusion protein) and a c200 construct (a fusion of the NS3 and NS3
 CC domains). This protein used in the construction of novel combinations of
 CC HCV antigens that have a broader range of immunological activity than any
 CC single HCV antigen. An example of such an antigen given in this
 CC specification comprises a first antigen containing at least 8 amino acids
 CC of the C domain of the HCV polyprotein and a second antigen comprising at
 CC least 8 amino acids of the NS3 domain, the NS4 domain, the S domain or
 CC the NS5 domain of the HCV polyprotein in the form of a fusion protein, a
 CC physical mixture or bound to a solid matrix
 XX
 SQ Sequence 1021 AA;
 Query Match 64.8%; Score 3829.5; DB 2; Length 1021;
 Best Local Similarity 67.2%; Pred. No. 5.2e-261;
 Matches 784; Conservative 24; Mismatches 79; Indels 279; Gaps 17;
 QY 1 MATKAVCVLKGDPVQGLINFEQKESNGPVKWSIKGLTEGLHGHVHFEFGDNTAGCTS 60
 DB 1 MATKAVCVLKGDPVQGLINFEQKESNGPVKWSIKGLTEGLHGHVHFEFGDNTAGCTS 60
 QY 61 AGPHFPLSRKKGKGPDEERHVGDLGNVTADKGVADSVIEDSVISLGDHCHIIIGRTLTV 120
 DB 61 AGPHFPLSRKKGKGPDEERHVGDLGNVTADKGVADSVIEDSVISLGDHCHIIIGRTLTV 120
 QY 121 HEKADDLGKGNNEESTKTGNAGSLACGVIGIAQNLNSGCNCSYIPGHITGHRMAWKLS 180
 DB 121 HEKADDLGKGNNEESTKTGNAGSLACGVIGIAQNLNLEFGA----- 160
 QY 181 AARTSGFVSLFAPGAKQNETHTVTGGAARTTSGLSLSPGASQNLQLIVDPIVENLE 240
 DB 161 -----VDFIPVENLE 170
 QY 241 TTRSRPVFTDSSPPVQSFQVAHLHAPVTSKSTKVPAAQAQGVKVLVNLPSVAATL 300
 DB 171 TTRSRPVFTDSSPPVQSFQVAHLHAPVTSKSTKVPAAQAQGVKVLVNLPSVAATL 230

QY 301 GFGAYMSKAGHIDPNIRTVGRTITITGSPITTYSTYCKFLADGCGSGAYDIIICDCHSTD 360
 DB 231 GFGAYMSKAGHIDPNIRTVGRTITITGSPITTYSTYCKFLADGCGSGAYDIIICDCHSTD 290
 QY 361 ATSLIGIGTGLDQAEATAGARLVVLATATPPGSGVTVPHPNIEVALSTTGEIPFYGKAIP 420
 DB 291 ATSLIGIGTGLDQAEATAGARLVVLATATPPGSGVTVPHPNIEVALSTTGEIPFYGKAIP 350
 QY 421 EVIKGRHLIFCHSKKCKDELAALVAGINAVAYRGLDVSIVPTSGDVVVVATDALMT 480
 DB 351 EVIKGRHLIFCHSKKCKDELAALVAGINAVAYRGLDVSIVPTSGDVVVVATDALMT 410
 QY 481 GYTGFDSVIDDNTCTVTQVDFSLDPTTETITIPQDAVSTORRGTRGKPGIYRFV 540
 DB 411 GYTGFDSVIDDNTCTVTQVDFSLDPTTETITIPQDAVSTORRGTRGKPGIYRFV 470
 QY 541 APGERPSGMFDSVLCBCYDAGCAWVELTPAETTVLRAYMNTPLPVCQDHLFEWGVF 600
 DB 471 APGERPSGMFDSVLCBCYDAGCAWVELTPAETTVLRAYMNTPLPVCQDHLFEWGVF 530
 QY 601 TGLTHIDAHFLSQTQSGENLPYLVAQATVCARQAQPPSWDMWKCLIRLKPILHGT 660
 DB 531 TGLTHIDAHFLSQTQSGENLPYLVAQATVCARQAQPPSWDMWKCLIRLKPILHGT 590
 QY 661 PLYRLGAVONEITLTHPVTKYIMTMSADLEVTIS----- 696
 DB 591 PLYRLGAVONEITLTHPVTKYIMTMSADLEVTIS----- 650
 QY 697 ----ACSGKPAIIPDREVLVREFDEMECSQHLPIYEQGMMLAEPKOKALGI-----SRG 748
 DB 651 VORVULSGKPAIIPDREVLVREFDEMECSQHLPIYEQGMMLAEPKOKALGI-----SRG 710
 QY 749 GKPAIVDPKVELVYQYD-----EMEECSQAAPYIEQAQVIAHQFKEKVLGLIDNDQVVVT 803
 DB 711 AE-VIAPAVQTNWQKLETFWAKHMNFISGIQYLAGLSTLPG--NPALIASLMAFTAATVS 767
 QY 804 P--DKELIYE-----AFDEMECSKAALIEECQRMALMKSIOGL 843
 DB 768 PLTTSQTLLENILGGMVAQAAPGAATAFVGAGLAGAAGSVGLGKVLIDILAGYAGV 827
 QY 844 LG-----ILRRHVGPGEAVQWNNEL 864
 DB 828 AGALVAFKIMSGEVSTEDLVNLLPAILSPGALVGVVCAAILRRHVGPGEAVQWNNEL 887
 QY 865 IAFASRGNHVSPHYVPSRSRRPAQALPYWARPDYNNPLVETWKKPDYBPVPHVHSGSSRR 924
 DB 888 IAFASRGNHVSP-----GNSST- 904
 QY 925 FAQALPVWARPDYNNPLVETWKKPDYEPVPHVHGRKTRNTNREPQDVKPPGGQIVG--- 981
 DB 905 -----NP-----KPO-----KKNKNTNRRPQDVKPPGGQIVGVV 936
 QY 982 ---RRGP-----PIPKARPEGRRTWAQPGYFWPLYGNK----- 1011
 DB 937 LUPRRGPRLGVRATRKTSERSQPRGRQPIPKARPEGRRTWAQPGYFWPLYGNCGGWAG 996
 QY 1012 ---DRESTGKSGKPGYWPWRKTRN 1034
 DB 997 WLLSPGRSPSWGPTD---PRRRSRN 1019
 RESULT 7
 AAE22050
 ID AAE22050 standard; protein; 1021 AA.
 XX
 AC AAE22050;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE pSOD/c200/core expression plasmid protein.
 XX
 KW Hepatitis C virus; HCV; antigen; C domain; polyprotein; NS3 domain;

NS4 domain; S domain; NS5 domain; pSOD/c200/core plasmid.

Hepatitis C virus.
Unidentified.
Chimeric.

Key Location/Qualifiers
1..154
/note= "hsod"
Region
155..159
/note= "Linker region"
Region
160..899
/note= "HCV c200"
Region
900..902
/note= "Linker region"
Region
903..1021
/note= "HCV c22"

US6312889-B1.

06-NOV-2001.

12-MAY-1995; 95US-00440549.

04-APR-1990; 90US-00504352.

07-JUL-1992; 92US-00910760.

(CHIR) CHIRON CORP.

Houghton M, Choo Q, Kuo G;

WPI; 2002-040268/05.

N-ESDB; AAD35044.

Combination of hepatitis C viral (HCV) antigens, useful in improved immunoassay for detecting HCV antibodies.

Example 6; Fig 4; 58pp; English.

The invention relates to combination of hepatitis C viral (HCV) antigens that have a broader range of immunological reactivity than any single HCV antigen. The combinations consist of an antigen from the C domain of the HCV polypeptide, and at least one additional HCV antigen from either the NS3 domain, the NS4 domain, the S domain, or the NS5 domain and are in the form of fusion protein, a simple physical mixture, or the individual antigens commonly bound to a solid matrix. The combinations of antigens provides broad range immunoassays for anti-HCV antibodies. The invention therefore provides a method for detecting antibodies to HCV in a mammal suspected of containing such antibodies. The present sequence is a protein encoded by pSOD/c200/core expression plasmid DNA containing HCV coding sequence

Sequence 1021 AA;

Query Match 64.8%; Score 3829.5; DB 5; Length 1021;
Best Local Similarity 67.2%; Pred. No. 5.2e-261;
Matches 784; Conservative 24; Mismatches 79; Indels 279; Gaps 17;

1 MATKAVCVLKGDPVQGIINFEQKESNGPVKWSIKGLTEGLGHGFVHVEFGDNTAGTS 60
1 MATKAVCVLKGDPVQGIINFEQKESNGPVKWSIKGLTEGLGHGFVHVEFGDNTAGTS 60
61 AGPHNPLSRKHGPKDDEHVGDLGNVTADKGVADVSIEDSVISLGDHCIIIGRTLV 120
61 AGPHNPLSRKHGPKDDEHVGDLGNVTADKGVADVSIEDSVISLGDHCIIIGRTLV 120
121 HEXADDLKGKNEESTKTGNAGSLACGVIGIAONLNSGCNSIYPHITGHRVANKLGS 180
121 HEXADDLKGKNEESTKTGNAGSLACGVIGIAONLNSGCNSIYPHITGHRVANKLGS 180
181 AARTTSFVSLFAPKQKETHVTGGAARTTSLTSLFSPGASQNIQLIVDFIPVENLE 240
161 -----VDIFIPVENLE 170

241 TTMRSPVFTDSSPPVPQSFQVAHLHAPTGSKSTKVPAAVAAOAGYKVLNPSVAATL 300
171 TTMRSPVFTDSSPPVPQSFQVAHLHAPTGSKSTKVPAAVAAOAGYKVLNPSVAATL 230
301 GFGYMSKAHGIDPNIRTVGRTITTTGSPITTYSTYKFLADGGCGSGAGYDIIICDCHSTD 360
231 GFGYMSKAHGIDPNIRTVGRTITTTGSPITTYSTYKFLADGGCGSGAGYDIIICDCHSTD 290
361 ATSLIGTIGTLDQAETAGARLVWLTATATPPSGVTVPHNIEVALSTTGEIPFYKAIPL 420
291 ATSLIGTIGTLDQAETAGARLVWLTATATPPSGVTVPHNIEVALSTTGEIPFYKAIPL 350
421 EVIKGGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSVIPDSGVVVVADALMT 480
351 EVIKGGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSVIPDSGVVVVADALMT 410
481 GYTGDFSDVIDCNTCVTQTVDFSLDPTFTIITLPQDAVSRTQRRGTGRGKPGIYRFV 540
411 GYTGDFSDVIDCNTCVTQTVDFSLDPTFTIITLPQDAVSRTQRRGTGRGKPGIYRFV 470
541 APGERPSGMFDSVLCYDAGCAYELTPAETTVLRLAYMNTPLGYPVCDHLEFEGVVF 600
471 APGERPSGMFDSVLCYDAGCAYELTPAETTVLRLAYMNTPLGYPVCDHLEFEGVVF 530
601 TGLTHIDAHFLSQTQKSGENLPYLVAOATVCARAQAPPPSWDQWKKLIRLKPFLHGTPT 660
531 TGLTHIDAHFLSQTQKSGENLPYLVAOATVCARAQAPPPSWDQWKKLIRLKPFLHGTPT 590
661 PLYRLGAVQNEITLTHPVTKYIMTMSADLEVVTIS----- 696
591 PLYRLGAVQNEITLTHPVTKYIMTMSADLEVVTIS----- 650
697 ---ACSKPAILIPREVLYREFDEMEECISOHLPIEQGMMLAQFKOKALGL-----SRG 748
651 VGRVVLGKPAIIPREVLYREFDEMEECISOHLPIEQGMMLAQFKOKALGL----- 710
749 GKPAIVDPKQVLYQOYD-----EMEECSQAAPYTHQAVIAHQFKEKVLGIDNDQVVVT 803
711 AE-VIAPAVQTNWQKLETFWAKHWNFISGTYLAGLSTLPG--NPATIASLMAFTAATVS 767
804 P---DKSEILYE-----AFDEMEHCASKAALIIEGQMAEMLKSKIOGL 843
768 PLTTTSQTLLENILGWVAAQLAAPCAATAFVAGLAGAAGSGLGKVLIDILAGYAGV 827
844 LG-----ILRRHYCPGSGAYQWMMNRL 864
828 AGALVAFKIMSGEVFPSTEDLVNLLPALISPGALVGVVCAAILRRHYCPGSGAYQWMMNRL 887
865 IAFASRGNHVSPTHYVPSRRRFAQALPVWARPDYNNPLVETWKKPDYEPVWVHRSRR 924
888 IAFASRGNHVSPT-----GNSST- 904
925 FAQALPVWARPDYNNPLVETWKKPDYEPVWVHRSRRFAQALPVWARPDYNNPLVETWKKPDYEPVWVHRSRR 981
905 -----NP-----KPQ-----KKKRNTRNRPDQVFKFPGGGQIVGVY 936
982 ---RRGP-----PIPKARPPSGRTWAOPGYKPMPLKGNK----- 1011
937 LLPRGPRGLGVRATKTSERSQPRGRQPIPKARPPSGRTWAOPGYKPMPLKGNK----- 996
1012 ---DRRSTGKSWGKPGYFVPRKTKRN 1034
997 WLLSPRGRPSWGPTD--FRRSRN 1019

RESULT 8

AAR68547

ID AAR68547 standard; protein; 841 AA.

XX AC AAR68547;

XX DT 25-MAR-2003 (revised)

CC useful in assaying and designing antiviral agents specific for HCV. The
CC method is used in identifying antiviral agents effective for treating
CC HCV. The present sequence is an HCV protease/hSOD fusion protein.
XX
XX
SQ Sequence 841 AA;

Query Match 51.6%; Score 3050.5; DB 7; Length 841;
Best Local Similarity 72.6%; Pred. No. 3.6e-206;
Matches 615; Conservative 10; Mismatches 37; Indels 185; Gaps 11;

QY 1 MATKAVCVLKGDGPVQGIINFEOKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
Db 1 MATNPVCVLKGDGPVQGIINFEOKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60

QY 61 AGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLTV 120
Db 61 PGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLTV 120

QY 121 HEKADDLGKGGNEESTKTGNAGSLACGVIGIAQNLNGCNCISIYPGHITGHR----- 173
Db 121 HEKADDLGKGGNEESTKTGNAGSLACGVIGIR-----IGTYVY-NHLTPLRDMAHNGL 174

QY 174 -----MAWLGSA-----RTTSGFVS----- 190
Db 175 RDLAVAVEPVFVSQMETKLIITWGAADTAACGDIINGLPVSARRGRIILGPADGMVSKGWR 234

QY 191 LFAP-----GAKONETH-----VTG 205
Db 235 LLAAPTAYAAQTRGLLGCIIITSLTGDKNOVEGEVQIVSTAQTFLATCIINGVCWTVVH 294

QY 206 GAAART-----TSGLT----- 216
Db 295 GAGTRTIASPKGEVIMQYTNVDLWGPASQGRSLTPTCTGSSDLXLVTRHADVIPVR 354

QY 217 -----SLFSP-----CAS-----QNIQLIVDRIPVENLET 241
Db 355 RRGDSRGLSLRPRTSYLKGSSGGLPCPAGHAGVIFRAAVCTRGVAKAVDIPVENLET 414

QY 242 TMRSPVFTNSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQGVKVLNPSVAATLG 301
Db 415 TMRSPVFTNSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQGVKVLNPSVAATLG 474

QY 302 FGAYMSKAHGIDPNIRGTVRTITGSPITYSTYTGKFLADGGCGGAYDIIICDECHSTDA 361
Db 475 FGAYMSKAHGIDPNIRGTVRTITGSPITYSTYTGKFLADGGCGGAYDIIICDECHSTDA 534

QY 362 TSILGIGTVLDQAETAGARLVLATATPPGSVTVPHNPTEEVALSTTGETIPRYGKALPLE 421
Db 535 TSILGIGTVLDQAETAGARLVLATATPPGSVTVPHNPTEEVALSTTGETIPRYGKALPLE 594

QY 422 VIKGGRHLIFCHSKKKDELAALKVALGINAVAYRGLDVSVIPTSQDVVVVATDALMTG 481
Db 595 VIKGGRHLIFCHSKKKDELAALKVALGINAVAYRGLDVSVIPTSQDVVVVATDALMTG 654

QY 482 YTGDFDSVIDNCVTQTVDFSLDPTFTTITILPDQAVSRTORRGTRGKGGIYRFVA 541
Db 655 YTGDFDSVIDNCVTQTVDFSLDPTFTTITILPDQAVSRTORRGTRGKGGIYRFVA 714

QY 542 PGRPSGMDSSVLCYDAGCAWYELTPAETTVRLRAYMNTPLGVPVCDHLEFEGVFT 601
Db 715 PGRPPGMFDSSVLCYDAGCAWYELTPAETTVRLRAYMNTPLGVPVCDHLEFEGVFT 774

QY 602 GLTHIDAHFLSQTQKSGENLPYLVAQATVCARAQAPPSPDQMWKCLIRLKPTELHGPTP 661
Db 775 GLTHIDAHFLSQTQKSGENLPYLVAQATVCARAQAPPSPDQMWKCLIRLKPTELHGPTP 834

QY 662 LLYRLGA 668
Db 835 LLYRLGA 841

ID AAW01701 standard; protein; 841 AA.
XX AC AAW01701;
XX 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 03-APR-1997 (first entry)
XX hSOD-HCV fusion protein.
XX HCV; NS3; non-structural domain 3; protease; polyprotein; inhibitor;
KW screen; processing; infection; treatment; probe; hepatitis C virus.
XX Hepatitis C virus; Virus.
OS Homo sapiens.
OS Chimeric.
XX Key Location/Qualifiers
FT Protein 156..841
FT /label= HCV_protease
XX US5585258-A.
XX 17-DEC-1996.
XX 06-DEC-1994; 94US-00350884.
XX 04-APR-1990; 90US-00505433.
XX 04-APR-1991; 91US-00680296.
XX (CHIR) CHIRON CORP.
XX Choo Q, Kuo G, Houghton M;
XX WPI; 1997-051175/05.
XX N-PSDB; AAT59261.
XX Compens. contg. hepatitis C virus NS3 domain protease and related fusion
PT proteins - useful for screening specific inhibitors, potential antiviral
PT agents, pregn. of antibodies and for cleaving specific poly:peptide(s).
XX Example 4; Col 77-84; 68pp; English.
XX Compens. comprising the hepatitis C virus (HCV) NS3 domain protease or
CC its active truncation analogues are claimed. Also new are fusion proteins
CC comprising the protease (or analogues) and, e.g. human superoxide (SOD)
CC or ubiquitin. The protease is essential for polyprotein processing, and
CC thus infectivity, in HCV. The compens. are used to screen for specific
CC inhibitors (possibly useful as antiviral agents), to generate specific
CC antibodies and to cleave specific polypeptides. HCV cDNA clones (AAT59250
CC - 56 encoding AAW01686-92 resp.) were isolated from HCV genomic library
CC using probes AAT59244-49. The clones were used in the preparation of full
CC -length SOD-protease fusion proteins. The present sequence is encoded by
CC vector cflSODp600 which contains a full-length HCV protease coding
CC sequence fused to a functional hSOD leader. The resulting vector encodes
CC amino acids 1-151 of hSOD, and amino acids 946-1630 of HCV (corresponding
CC to 1-686 of AAW01693). (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 17-OCT-2003 to standardise OS field)

Sequence 841 AA;

Query Match 51.5%; Score 3047.5; DB 2; Length 841;
Best Local Similarity 72.6%; Pred. No. 5.9e-206;
Matches 615; Conservative 9; Mismatches 38; Indels 185; Gaps 11;

QY 1 MATKAVCVLKGDGPVQGIINFEOKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
Db 1 MATNPVCVLKGDGPVQGIINFEOKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60

QY 61 AGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLTV 120
Db 61 PGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLTV 120

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QY 121 HEKADDLKGGNEESTKTGNAGSRLACGVIGIAQNLSGNCSTIYPGHITGHR-----173
Db |||||
QY 121 HEKADDLKGGNEESTKTGNAGSRLACGVIGIR-----GTVVY-NHLTPLRDWAHNL 174
Db |||||
QY 174 -----MAWKLGSAA-----RTSGFVS-----190
Db |||||
QY 175 RDLAVAVEPVFSQMETKLITWGADTAACDIIINGLPVSARRGRILLGPADGMVSKGWR 234
Db |||||
QY 191 LFAP-----GAKONETH-----VTG 205
Db |||||
QY 235 LLAPITAYAAQTRGLLGCIIITSLTRDKNOVGEVQIVSTAQTFLATCIINGVCWTYH 294
Db |||||
QY 206 GAAART-----TSGLT-----216
Db |||||
QY 295 GAGTRTIASPKGPVIQMYTNVDQDLVGWPASQGTSLTPTCTCGSSDLYLVRHADVIPVR 354
Db |||||
QY 217 -----SLFSP-----CAS-----217
Db |||||
QY 355 RRGDSRGSLLSPRIISYLGSSGGPLPCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 414
Db |||||
QY 242 TMRSPVFTDSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAVAAQYKVLNPSVAATLG 301
Db |||||
QY 415 TMRSPVFTDSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAVAAQYKVLNPSVAATLG 474
Db |||||
QY 302 FGAYMSKAHGIDPNIRTVGRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDA 361
Db |||||
QY 475 FGAYMSKAHGIDPNIRTVGRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDA 534
Db |||||
QY 362 TSIIGIGVLDQAEATAGARLVATATPPGSVTVPHNIEEVALSTTGEIPFYKAIPL 421
Db |||||
QY 535 TSIIGIGVLDQAEATAGARLVATATPPGSVTVPHNIEEVALSTTGEIPFYKAIPL 594
Db |||||
QY 422 VIKGRHLIFCHSKKKCDLAALKVALGINAVAYRGLDVSIVPTSGDWWVATDALTG 481
Db |||||
QY 595 VIKGRHLIFCHSKKKCDLAALKVALGINAVAYRGLDVSIVPTSGDWWVATDALTG 654
Db |||||
QY 482 YTGDFDSVIDNCTVQTQVDFSLDPTFTIETITLQDAVSTQRRGTRGKPGIYRVA 541
Db |||||
QY 655 YTGDFDSVIDNCTVQTQVDFSLDPTFTIETITLQDAVSTQRRGTRGKPGIYRVA 714
Db |||||
QY 542 PGERPFGMFDSSVLCECYDAGCAMELTTPAETTVLRAYMNTPGLPYCODHLEFWEVFT 601
Db |||||
QY 715 PGERPFGMFDSSVLCECYDAGCAMELTTPAETTVLRAYMNTPGLPYCODHLEFWEVFT 774
Db |||||
QY 602 GLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSDQWKKLIRLKPILHGTTP 661
Db |||||
QY 775 GLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSDQWKKLIRLKPILHGTTP 834
Db |||||
QY 662 LLYRLGA 668
Db |||||
QY 835 LLYRLGA 841
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RESULT 12

AAW46397
ID AAW46397 standard; protein; 841 AA.

AC AAW46397;

DT 27-AUG-2003 (revised)

TX 07-MAY-1998 (first entry)

DE Amino acid sequence of the vector cf1SODp600.

XX Protease; HCV; NS3 domain; human superoxide dismutase; fusion protein;
KW assay; activity; anti-HCV.

OS Synthetic.

OS Hepatitis C virus.

OS Homo sapiens.

FN US5712145-A.

XX

PD 27-JAN-1998.
XX 06-SEP-1996; 96US-00709173.
XX 04-APR-1990; 90US-00505433.
PR 04-APR-1991; 91US-00680296.
PR 06-DEC-1994; 94US-00350884.
PR 12-MAY-1995; 95US-00440548.
XX (CHIR) CHIRON CORP.
XX Choo Q, Kuo G, Houghton M;
PI WPI: 1998-111986/11.
XX N-PSDB; AAV04993.
DR Recombinant hepatitis C virus protease - useful in screening drugs for
PT activity against hepatitis C virus.
XX Disclosure; Fig 10A-G; 68pp; English.
XX The present sequence represents the amino acid sequence of the vector
CC cf1SODp600. This vector contains a full length Hepatitis C virus (HCV)
CC protease coding sequence fused to a functional human superoxide dismutase
CC leader. The vector was used to express the protease fusion protein in
CC Escherichia coli. The HCV protease is believed to cleave itself from the
CC genomic polyprotein. In the absence of protease activity, the HCV
CC polyprotein should remain in its unprocessed form, and thus render the
CC virus non-infectious. Inhibitors of protease activity should also inhibit
CC viral infectivity. The protease can therefore be used for assaying
CC compounds for activity against HCV. (Updated on 27-AUG-2003 to correct OS
XX field.)
SQ Sequence 841 AA;

Query Match 51.5%; Score 3047.5; DB 2; Length 841;
Best Local Similarity 72.6%; Pred. No. 5.9e-206;
Matches 615; Conservative 9; Mismatches 38; Indels 185; Gaps 11;
QY 1 MATKAVCVLKDGVPQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
Db |||||
QY 1 MATNPVCVLKDGVPQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
Db |||||
QY 61 AGPHFNPLSRKHGPKDERHVGDLGNVTADKGVADVSDIEDSVISLSDHCHIIIGRTLV 120
Db |||||
QY 61 PGPHFNPLSRKHGPKDERHVGDLGNVTADKGVADVSDIEDSVISLSDHCHIIIGRTLV 120
Db |||||
QY 121 HEKADDLKGGNEESTKTGNAGSRLACGVIGIAQNLSGNCSTIYPGHITGHR-----173
Db |||||
QY 121 HEKADDLKGGNEESTKTGNAGSRLACGVIGIR-----GTVVY-NHLTPLRDWAHNL 174
Db |||||
QY 174 -----MAWKLGSAA-----RTSGFVS-----190
Db |||||
QY 175 RDLAVAVEPVFSQMETKLITWGADTAACDIIINGLPVSARRGRILLGPADGMVSKGWR 234
Db |||||
QY 191 LFAP-----GAKONETH-----VTG 205
Db |||||
QY 235 LLAPITAYAAQTRGLLGCIIITSLTRDKNOVGEVQIVSTAQTFLATCIINGVCWTYH 294
Db |||||
QY 206 GAAART-----TSGLT-----216
Db |||||
QY 295 GAGTRTIASPKGPVIQMYTNVDQDLVGWPASQGTSLTPTCTCGSSDLYLVRHADVIPVR 354
Db |||||
QY 217 -----SLFSP-----CAS-----217
Db |||||
QY 355 RRGDSRGSLLSPRIISYLGSSGGPLPCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 414
Db |||||
QY 242 TMRSPVFTDSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAVAAQYKVLNPSVAATLG 301
Db |||||
QY 415 TMRSPVFTDSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAVAAQYKVLNPSVAATLG 474
Db |||||
QY 302 FGAYMSKAHGIDPNIRTVGRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDA 361
Db |||||

Db 475 FGAYMSKAHGIDPNIRTVGRTITTSPTITSTYTKFLADGGCGGAYDIIICDECHSTDA 534
 QY 362 TSILGIGTVLDOAETAGARLVLAATATPPGVTVPHPNIEEVALSTTGEIIPFYKAIPL 421
 Db 535 TSILGIGTVLDOAETAGARLVLAATATPPGVTVPHPNIEEVALSTTGEIIPFYKAIPL 594
 QY 422 VIKGGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSVIPSGDVVVVATDALMTG 481
 Db 595 VIKGGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSVIPSGDVVVVATDALMTG 654
 QY 482 YTGDFSDVIDCNTCTVTQTVDFSLDPTFTTETITLPODAVSRTOGRGKPGIYRFA 541
 Db 655 YTGDFSDVIDCNTCTVTQTVDFSLDPTFTTETITLPODAVSRTOGRGKPGIYRFA 714
 QY 542 PGERPSGMFDSVLCEDYDAGCAWYELPAETTVRLRAYMNTPLPVCQDHLFEWGVFT 601
 Db 715 PGERPSGMFDSVLCEDYDAGCAWYELPAETTVRLRAYMNTPLPVCQDHLFEWGVFT 774
 QY 602 GLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLPTLHGPTP 661
 Db 775 GLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLPTLHGPTP 834
 QY 662 LLYRLGA 668
 Db 835 LLYRLGA 841

RESULT 13

AAW97609
 ID AAW97609 standard; protein; 841 AA.

XX AC AAW97609;

XX DT 26-MAY-1999 (first entry)

XX DE Amino acid sequence of vector cflSODp600.

XX KW HCV NS3 protease; truncation analog; HCV control; protease activity;
 viral infectivity; inactive non-cleaving protease.

XX OS Synthetic.

XX OS Hepatitis C virus.

XX PN US5885799-A.

XX PD 23-MAR-1999.

XX PF 06-SEP-1996; 96US-00709177.

XX PR 04-APR-1990; 90US-00505433.

XX PR 04-APR-1991; 91US-00680296.

XX PR 06-DEC-1994; 94US-00350884.

XX PR 12-MAY-1995; 95US-0040548.

XX PA (CHIR) CHIRON CORP.

XX PI Choo Q, Kuo G, Houghton M;

XX PI WPI; 1999-228536/19.

XX DR N-PSDB; AAX26398.

XX DR Preparation of new Hepatitis C Virus NS3 protease - useful for screening
 for compounds which inhibit HCV infectivity.

XX PS Example 3; Fig 10; 71pp; English.

XX CC The specification describes a method for making a purified Hepatitis C
 virus (HCV) NS3 protease or active truncation analog. If the HCV protease
 C-terminal cleavage signal is excluded (so that self-cleavage is
 prevented), the HCV protease remains in its unprocessed form, and renders
 the virus noninfectious. The protease is therefore useful for assaying
 pharmaceutical agents for control of HCV, as compounds which inhibit
 protease activity sufficiently will also inhibit viral infectivity. An

CC inactive non-cleaving protease can be used to screen for inhibitors.
 CC Recombinant expression systems can be utilised to prepare recombinant HCV
 CC which can be used to produce monoclonal antibodies. The present sequence
 CC was created in the course of the invention

XX SQ Sequence 841 AA;

Query Match 51.5%; Score 3047.5; DB 2; Length 841;

Best Local Similarity 72.6%; Pred. No. 5.9e-206;

Matches 615; Conservative 9; Mismatches 38; Indels 185; Gaps 11;

QY 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVHFEFNDTAGCTS 60

Db 1 MAINPVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVHFEFNDTAGCTS 60

QY 61 AGPHFNPLSRKHGGPKDEERHVGDLGNVTADKGVADVSDIESVLSGDHCICIIGRTLVV 120

Db 61 PGPHFNPLSRKHGGPKDEERHVGDLGNVTADKGVADVSDIESVLSGDHCICIIGRTLVV 120

QY 121 HEKADDLKGGNEESTKTNAGSRLACGVIGTAQNLNSGCNCIYPGHTGHR----- 173

Db 121 HEKADDLKGGNEESTKTNAGSRLACGVIGIR-----GTYYV-NHLTPLRDWAHNL 174

QY 174 -----MAWKLGSAA-----RTTSGFVS----- 190

Db 175 RDLAVAVEPVFSQMETKLIITWGAATACGDIINGLIPVSARRGRELLGPDAGMYSKWR 234

QY 191 LFAP-----GAKQNETH-----VTG 205

Db 235 LLAPITAYAAQTRGLLGLCIITSLTGRDNQVEGEVQIVSTAQTFLATCIINGVCVTVYH 294

QY 206 GAAART-----TSGLT----- 216

Db 295 GAGTRTIASPKGEVIMQYTNVDQLVGMWPAISOQTRSLTPTCTCGSSDLXIVTRHADVIPVR 354

QY 217 -----SLFSP-----GAS-----QNTQLIVDFIPVENLET 241

Db 355 RRGDSRGLSLSPRISYILKSGSGGLPCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 414

QY 242 TMRSPVFTDNSSPPVVPVQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPNSVAATLG 301

Db 415 TMRSPVFTDNSSPPVVPVQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPNSVAATLG 474

QY 302 FGAYMSKAHGIDPNIRTVGRTITTSPTITSTYTKFLADGGCGGAYDIIICDECHSTDA 361

Db 475 FGAYMSKAHGIDPNIRTVGRTITTSPTITSTYTKFLADGGCGGAYDIIICDECHSTDA 534

QY 362 TSILGIGTVLDOAETAGARLVLAATATPPGVTVPHPNIEEVALSTTGEIIPFYKAIPL 421

Db 535 TSILGIGTVLDOAETAGARLVLAATATPPGVTVPHPNIEEVALSTTGEIIPFYKAIPL 594

QY 422 VIKGGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSVIPSGDVVVVATDALMTG 481

Db 595 VIKGGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSVIPSGDVVVVATDALMTG 654

QY 482 YTGDFSDVIDCNTCTVTQTVDFSLDPTFTTETITLPODAVSRTOGRGKPGIYRFA 541

Db 655 YTGDFSDVIDCNTCTVTQTVDFSLDPTFTTETITLPODAVSRTOGRGKPGIYRFA 714

QY 542 PGERPSGMFDSVLCEDYDAGCAWYELPAETTVRLRAYMNTPLPVCQDHLFEWGVFT 601

Db 715 PGERPSGMFDSVLCEDYDAGCAWYELPAETTVRLRAYMNTPLPVCQDHLFEWGVFT 774

QY 602 GLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLPTLHGPTP 661

Db 775 GLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLPTLHGPTP 834

QY 662 LLYRLGA 668

Db 835 LLYRLGA 841

RESULT 14

AAR14349	DB	ACTRTIASPKGPVIOMYINVDQDLVGPASQCTRLTCTCGSSDLVLTVRHADVIPVR	354
ID AAR14349 standard; protein; 840 AA.			
AC AAR14349;			
XX			
DT 16-JAN-1992 (first entry)			
XX			
DE HCV protease::hSOD leader fusion encoded by cfISODp600.			
XX			
KW Hepatitis C virus; HCV; human superoxide dismutase; SOD.			
XX			
OS Hepatitis C virus.			
XX			
FT Key			
FT Region			
FT Protein			
FT			
XX			
FN W09115596-A.			
XX			
PD 17-OCT-1991.			
XX			
PF 04-APR-1990; 90US-00505434.			
XX			
PR 04-APR-1990; 90US-00505434.			
XX			
PA (PROT-) PROTOS INC.			
XX			
PI Rosenbergs S;			
XX			
DR WPI; 1991-325236/44.			
DR N-PSDB; AAQ14358.			
XX			
PT Method for assaying pharmaceutical cnds. - for determining anti-Hepatitis			
PT C Virus activity, using binding affinity.			
XX			
PS Example 4; Fig 10; 68pp; English.			
XX			
CC The vector cfISODp600 contains a full-length HCV protease coding sequence			
CC fused to a functional hSOD leader. The truncated protease analogue			
CC expressed by the vector is proteolytically inactive and can be used to			
CC assay a wide range of pharmaceutical agents for controlling HCV. Those			
CC agents which inhibit the protease activity sufficiently will also inhibit			
CC viral infectivity. See also AAR14350-R14356			
XX			
SQ Sequence 840 AA;			
Query Match	51.5%;	Score 3042.5;	DB 2; Length 840;
Best Local Similarity	72.6%;	Pred. No. 1.3e-205;	
Matches 614;	Conservative 9;	Mismatches 38;	Indels 185; Gaps 11;
QY 2 ATKAVCVLKGDPVQGIINFQKESNGPVKVGSTIKGLTEGLHGFHVEFGDNTAGCTSA 61			
DB 1 ATNFCVCLKGDPVQGIINFQKESNGPVKVGSTIKGLTEGLHGFHVEFGDNTAGCTSP 60			
QY 62 GPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVISLSDHCHIIIGRTLVVH 121			
DB 61 GPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVISLSDHCHIIIGRTLVVH 120			
QY 122 EKADDLKGKNEESTKTNAGSRACGVIGTAQNLNCGNCSTIYPGHITGHR----- 173			
DB 121 EKADDLKGKNEESTKTNAGSRACGVIGIR-----GTYYV-NHLTPLRDWAHNGLR 174			
QY 174 -----MAWKLGSAA-----RTTSGFVS-----L 191			
DB 175 DLAVAVEPVFVSQMETKLTWAGDTAACGDIINGLPVSARRGREILLGPADGMVSKGWR 234			
QY 192 FAP-----GAKQNEH-----VTGG 206			
DB 235 LAPITAYAQOTRGLGCIITSLTRDKNQVGEVQIVSTAAQTFLATCIINGVCMWTVVHG 294			
QY 207 AARET-----TSGLT----- 216			
DB 295 ACTRTIASPKGPVIOMYINVDQDLVGPASQCTRLTCTCGSSDLVLTVRHADVIPVR 354			
QY 217 -----SLFSP-----GAS-----ONTQLIVDFIPEVENLETT 242			
DB 355 RGDSSGSLSPRPISYLGKSGGPGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPEVENLETT 414			
QY 243 MESPVTDNSSPPVQSFQVVAHLHAPTSGSGSTKVPAAAYAAQGYKVLVNFPSVAATLGF 302			
DB 415 MESPVTDNSSPPVQSFQVVAHLHAPTSGSGSTKVPAAAYAAQGYKVLVNFPSVAATLGF 474			
QY 303 GAYMSKAHGIDPNIRTGVRTITITGSPITYSTYKGLADGGCGGAYDIIICDECHSTDA 362			
DB 475 GAYMSKAHGIDPNIRTGVRTITITGSPITYSTYKGLADGGCGGAYDIIICDECHSTDA 534			
QY 363 SILGIGTVLDQAETAGARLVVLAATATPPGSVTVPHNIEEVALSTGTGPIFYKGAIPLEV 422			
DB 535 SILGIGTVLDQAETAGARLVVLAATATPPGSVTVPHNIEEVALSTGTGPIFYKGAIPLEV 594			
QY 423 IKGGRHLIFCHSKKCCDELAALVALGINAVAYEGLDVSVIPTSGDVVVVATDALMTGY 482			
DB 595 IKGGRHLIFCHSKKCCDELAALVALGINAVAYEGLDVSVIPTSGDVVVVATDALMTGY 654			
QY 483 TGDPSVIDCNTCVTQTVDPSLDPTFTTITLPQDAVSRTOQRGRTGRKPGIYRFVAP 542			
DB 655 TGDPSVIDCNTCVTQTVDPSLDPTFTTITLPQDAVSRTOQRGRTGRKPGIYRFVAP 714			
QY 543 GERPGMFDSSVLCEDYDAGCAWYELTPAETTVRLRAYMNTFGLPVCODHLEFWEGVFTG 602			
DB 715 GERPGMFDSSVLCEDYDAGCAWYELTPAETTVRLRAYMNTFGLPVCODHLEFWEGVFTG 774			
QY 603 LTHIDAHFLSOTKSGENLPYLVAQATVCARAQAPPSNDOMWKCLRLKPTLHGPTPL 662			
DB 775 LTHIDAHFLSOTKSGENLPYLVAQATVCARAQAPPSNDOMWKCLRLKPTLHGPTPL 834			
QY 663 LYRLGA 668			
DB 835 LYRLGA 840			
RESULT 15			
AAP90164			
ID AAP90164 standard; protein; 2261 AA.			
XX			
AC AAP90164;			
XX			
DT 25-MAR-2003 (revised)			
DT 01-NOV-1989 (first entry)			
XX			
DE Peptide encoded by composite hepatitis C virus cDNA.			
XX			
KW Hepatitis C virus; clone 12f; clone 15e; probe; vaccine.			
XX			
OS Pan troglodytes.			
XX			
FN GB2212511-A.			
XX			
PD 26-JUL-1989.			
XX			
PF 18-NOV-1988; 88GB-00027024.			
XX			
PR 18-NOV-1987; 87US-00122714.			
PR 30-DEC-1987; 87US-00139886.			
PR 26-FEB-1988; 88US-00161072.			
PR 26-OCT-1988; 88US-00263584.			
XX			
FA (CHIR) CHIRON CORP.			
XX			
PI Houghton M, Choo QL, Kuo G;			
XX			
DR WPI; 1989-215054/30.			
DR N-PSDB; AAN90331.			
XX			

PT Hepatitis C virus gene - used for prodn. of polynucleotide probes
PT polypeptide(s) and antibodies for diagnosis, prevention and treatment of
PT infection.
XX
XX Disclosure; Fig 32; 30pp; English.
XX
XX The sequence is the peptide encoded by the composite hepatitis C virus
CC (HCV) cDNA of AAN90331. The polypeptides are used to diagnose HCV-induced
CC NANBH, to raise antibodies for immunoassay or treatment, or to produce
CC vaccines. (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 2261 AA;
SQ

Query Match 49.2%; Score 2309.5; DB 1; Length 2261;
Best Local Similarity 53.3%; Pred. No. 1.3e-195;
Matches 522; Conservative 33; Mismatches 92; Indels 419; Gaps 16;
224 SQNIQLIVDFIPVENLETTMRSPVTDNSPPVQSFQVAHLHAPTSGSKTKVPAAYA 283
:: :
561 TRGAKAVDFIPVENLETTMRSPVTDNSPPVQSFQVAHLHAPTSGSKTKVPAAYA 620
284 AQGYKVLNPSVAATLGFAGYMSKAHGIDPNIRGVRTITTTGSPITYSTYCKFLADGGC 343
621 AQGYKVLNPSVAATLGFAGYMSKAHGIDPNIRGVRTITTTGSPITYSTYCKFLADGGC 680
344 SGGAYDIIICDCHSTDATSIIGIGVLQDAQTAGARLVLTATATPPGSVTVPHNIEV 403
681 SGGAYDIIICDCHSTDATSIIGIGVLQDAQTAGARLVLTATATPPGSVTVPHNIEV 740
404 ALSTGTEIPFYGKAIPLEVIKGRHLIFCHSKKKDELAALKVALGINAVAYRGLDVSV 463
741 ALSTGTEIPFYGKAIPLEVIKGRHLIFCHSKKKDELAALKVALGINAVAYRGLDVSV 800
464 IPTSGDVVVVATDALMTGVTGDFDSVIDCNTCVTQVDFSLDPTFTIETITLPQDAVSRT 523
801 IPTSGDVVVVATDALMTGVTGDFDSVIDCNTCVTQVDFSLDPTFTIETITLPQDAVSRT 860
524 QRRGRTGRGKPGIYRFVAFGERPSGMFSDSVLCECYDAGCAMEYELTPAETTVLRAYMNT 583
861 QRRGRTGRGKPGIYRFVAFGERPSGMFSDSVLCECYDAGCAMEYELTPAETTVLRAYMNT 920
584 PGLPVCQDHLIEWEGVFTGLTHIDAFHLSQTKSGENLPYLVAQATVCARAQAPPSWD 643
921 PGLPVCQDHLIEWEGVFTGLTHIDAFHLSQTKSGENLPYLVAQATVCARAQAPPSWD 980
644 QMWKCLIRLKP TLHGPTLLYRLGAVONEITLTHPVTKYIMTCSADLEWVTS - 696
981 QMWKCLIRLKP TLHGPTLLYRLGAVONEITLTHPVTKYIMTCSADLEWVTSVVLVGG 1040
697 - - - - - ACSGKPAIIPDREVLRYREFDEMEBCSOHLPYIEQGMMLA 735
1041 VLAALAAYCLSTGCVVIVGRVWLSGKPAIIPDREVLRYREFDEMEBCSOHLPYIEQGMMLA 1100
736 EQFKQKALGL - - - - - SRGKPAIVPDKEVLVQYD - - - - - EMESCSQAAPYIEQAQVIAHQ 786
1101 EQFKQKALGLQATASQAE - VIAPAVQTNQCKLETFWAKHWNFIQGIQYLAGLSTLPG - 1158
787 FKEKVLGLDNDQVWVTP - - - - - DKEILYE - - - - - APDEMEECASKAALI 826
1159 - NPAIASLMAFTAAVTSPLTSTQTLLENILGGWVAQAAPGAATAFVGAGLAGAIGSV 1217
827 EEGORMAELMSKIQGLLG - - - - - IL 847
1218 GLGKVLIDILAGYGAGVAGALVAFKIMSGEVPSSTEDLVNLLPAILSPGALWGVVCAAIL 1277
848 RRHVGPGEVAVQWNNRLIAFASRGNHVSPHYVPS - - - - - 882
1278 RRHVGPGEVAVQWNNRLIAFASRGNHVSPHYVPSDAAARVTAISSLTIVTQLRLRHQ 1337
883 - - - - - 882
1338 WISSECTPCSGSWLRDINDWICEVLSDFKTLWKAKLMPQLGIPFVSCQGYKGVNRVD 1397

QY 883 ----- 882
Db 1398 GIMETRCHGAEITGHVKNGTMRIVGPRTCENMWSGTFPINAYTTGCTPLPAPNYTAL 1457
QY 883 -----RSRFA----- 888
Db 1458 WRVSABEYVEIROVGDPHYVTGMTTDLNLCQCPQVPSPEFFTELDGVRLHREAPPCKPLLR 1517
QY 889 -----QALPVWAPDY-----NPP----- 902
Db 1518 EEVSFVGLHEYPVGSQLPCEPEPDVAVLTSMLTDPHSHTAAAGRRLARLARGSPPSVASS 1577
QY 903 -----LVET---WKK-----PDYPPVVH 918
Db 1578 ASQLSAPSLKATCTANHSDPAELIEANLLWRQEMGNITRVESKVVILDSFDELVAE 1637
QY 919 G-----RSSRFAQALPVWAPDYNNPPLVETWKKPDYPPVHVHGXKTKRNTNR 966
Db 1638 EDEREISVPAELIRKSRFAQALPVWAPDYNNPPLVETWKKPDYPPVVH----- 1687
QY 967 RPQDVKFFGGGQIVGRRGPPPKARR 992
Db 1688 -----GCELPKPKSPVPPPRK 1704

Search completed: June 21, 2004, 10:30:26
Job time : 73.5868 secs

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OM protein - protein search, using sw model

Run on: June 21, 2004, 10:18:09 ; Search time 49.4736 Seconds
(without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-4
Perfect score: 4455
Sequence: 1 MATKAVCVLKGDPVQGIIN.....GNKRRRTGSKWGKPGYMP 829

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4455	100.0	829	AAE18690	Multiple
2	4455	100.0	829	ADC06769	Chimeric
3	4032	90.5	1099	Aau76378	HCV multi
4	4032	90.5	1099	Abg72262	HCV multi
5	2222	49.9	1021	Aaw34481	HCV antig
6	2222	49.9	1021	Aaw40039	Fusion pr
7	2222	49.9	1021	Aae22050	PSOD/c200
8	1627.5	36.5	1766	Aap92041	Hepatitis
9	1624.5	36.5	2261	Aap90164	Peptide e
10	1624.5	36.5	2436	AAP92050	Sequence
11	1624.5	36.5	2436	AAP90288	Peptide e
12	1624.5	36.5	2772	AAB18540	Protein e
13	1624.5	36.5	2955	AAV14975	Amino aci
14	1624.5	36.5	2955	AAV14975	Amino aci
15	1624.5	36.5	3011	AAV14975	Amino aci
16	1624.5	36.5	3011	AAV14975	Amino aci
17	1624.5	36.5	3011	AAV14975	Amino aci
18	1624.5	36.5	3011	AAV14975	Amino aci
19	1624.5	36.5	3011	AAV14975	Amino aci
20	1623	36.4	781	AAE18690	Multiple
21	1623	36.4	781	AAE18690	Multiple
22	1623	36.4	781	AAE18690	Multiple
23	1623	36.4	781	AAE18690	Multiple
24	1623	36.4	781	AAE18690	Multiple
25	1623	36.4	781	AAE18690	Multiple

26	1623	36.4	781	4	AAE18690	standard; protein; 829 AA.
27	1622.5	36.4	3011	5	AAU84597	HCV polyp
28	1621.5	36.4	2301	1	AAP92047	Sequence
29	1621.5	36.4	2772	2	AAE08123	Hepatitis
30	1619.5	36.4	2894	2	AAE24440	Composite
31	1616.5	36.3	2816	2	AAE34009	HCV-1 pol
32	1615.5	36.3	2435	2	AAE25135	HCV polyp
33	1614.5	36.2	2894	2	AAE70230	Composite
34	1614.5	36.2	3011	2	AAE31621	Hepatitis
35	1608.5	36.1	2436	2	AAE28582	HCV amino
36	1605.5	36.0	1786	1	AAE90158	Protein s
37	1600.5	35.9	2955	2	AAE08124	Hepatitis
38	1597.5	35.9	2202	6	AAE26783	Protein d
39	1597.5	35.9	2631	6	AAE26785	Protein d
40	1597.5	35.9	2984	4	AAE00442	Hepatitis
41	1597.5	35.9	3011	2	AAE40120	HCV genom
42	1597.5	35.9	3011	2	AAE77397	Hepatitis
43	1597.5	35.9	3011	2	AAE77398	Hepatitis
44	1597.5	35.9	3011	2	AAE98021	Infectiou
45	1597.5	35.9	3011	2	AAE98020	Infectiou

ALIGNMENTS

RESULT 1
AAE18690
ID AAE18690 standard; protein; 829 AA.
XX
AC AAE18690;
XX
DT 17-MAY-2002 (first entry)
XX
DE Multiple epitope fusion antigen (MEFA) 12 protein.
XX
KW Hepatitis C virus; NS3/4a antigen; multiple epitope fusion antigen;
KW HCV infection; MEFA 12 protein.
XX
OS Unidentified.

Key Location/Qualifiers
FH Misc-difference 315 /note= "Encoded by ATG"
FT Misc-difference 645 /note= "Encoded by GAG"
FT Misc-difference 645 /note= "Encoded by GAG"
XX
PN WO200196875-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US019369.
XX
PR 15-JUN-2000; 2000US-0212082P.
XX
PR 02-APR-2001; 2001US-0280811P.
XX
PR 02-APR-2001; 2001US-0280867P.
XX
(CHIR) CHIRON CORP.

Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
Medina-Selby A;
WPI; 2002-179522/23.
N-PSDB; AAD29796.

Immunassay solid support useful for detecting hepatitis C virus
infection in a biological sample, comprises at least one of HCV anti-core
antibody and HCV NS3/4a epitope, bound to the support.
Disclosure; Fig 7; 87pp; English.
The present invention relates to hepatitis C virus (HCV) core antigen and
NS (nonstructural) 3/4a antibody combination assay that can detect both
HCV antigens and antibodies present in a sample using a single solid

CC matrix as well as immunoassay solid supports for use in the assay. The
CC solid support is useful for detecting HCV infection in a biological
CC sample. The present sequence is MEFA (multiple epitope fusion antigen) 12
CC protein. This sequence is used in the exemplification of the invention
XX
SQ Sequence 829 AA;
Query Match 100.0%; Score 4455; DB 5; Length 829;
Best Local Similarity 100.0%; Pred. No. 1.7e-310; Indels 0; Gaps 0;
Matches 829; Conservative 0; Mismatches 0;
QY 1 MATKAVCVLKGDGPVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
DB 1 MATKAVCVLKGDGPVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
QY 61 AGPHFNPLSTRGCNCSIYPGHITGHRMAWKLGSAAARTTSGFVSLFAPGAKQNETHVTTGGA 120
DB 61 AGPHFNPLSTRGCNCSIYPGHITGHRMAWKLGSAAARTTSGFVSLFAPGAKQNETHVTTGGA 120
QY 121 AARTTSGLTSLFSPGASONIQLITSDNNSPPVQSFQVAHLHAPTGSKSTKVPAAAYA 180
DB 121 AARTTSGLTSLFSPGASONIQLITSDNNSPPVQSFQVAHLHAPTGSKSTKVPAAAYA 180
QY 181 AAGYKVLVLPNSVAATLGFAGYMSKAHGIDPNIRITGVRTITITGSPITYSTYKFLADGGC 240
DB 181 AAGYKVLVLPNSVAATLGFAGYMSKAHGIDPNIRITGVRTITITGSPITYSTYKFLADGGC 240
QY 241 SGGAYDIIICDECHSTATSIILGTVDQARTAGARLVLATATPGSVTVPHNIEEV 300
DB 241 SGGAYDIIICDECHSTATSIILGTVDQARTAGARLVLATATPGSVTVPHNIEEV 300
QY 301 ALSTGTGEPFVGKAIPLVIVKGRHLIFCHSKKCDLAAKLVALGINAVAYVYRGLDVSV 360
DB 301 ALSTGTGEPFVGKAIPLVIVKGRHLIFCHSKKCDLAAKLVALGINAVAYVYRGLDVSV 360
QY 361 IPTSGDVVVATDALMTGYTDFDSDVIDCNTACSGKPAIIPDREVLVYREFDEMECSQH 420
DB 361 IPTSGDVVVATDALMTGYTDFDSDVIDCNTACSGKPAIIPDREVLVYREFDEMECSQH 420
QY 421 LPYTEQGMMLAEQFKALGSLRGKPAIVDPKEVLVYQYDEMECSQAAPYIIEQAQVIA 480
DB 421 LPYTEQGMMLAEQFKALGSLRGKPAIVDPKEVLVYQYDEMECSQAAPYIIEQAQVIA 480
QY 481 HOFKEKVLGLDNDQVVVTPDKEILYEAFDMEECASKAALIEGQRMALMSKIQGLL 540
DB 481 HOFKEKVLGLDNDQVVVTPDKEILYEAFDMEECASKAALIEGQRMALMSKIQGLL 540
QY 541 GILRRHVGPGEGAVQWMNRLIAFASRGNHVSPTHYVPSRRRFAQALPVWARPDPYNPPLV 600
DB 541 GILRRHVGPGEGAVQWMNRLIAFASRGNHVSPTHYVPSRRRFAQALPVWARPDPYNPPLV 600
QY 601 ETWKKPDYEPVHVGRSSRRFAQALPVWARPDPYNPPLVETWKKPDYEPVHVGRKTKENT 660
DB 601 ETWKKPDYEPVHVGRSSRRFAQALPVWARPDPYNPPLVETWKKPDYEPVHVGRKTKENT 660
QY 661 NRRPDQVFPGGQIIVGGVILLPRRGLRLVLAATKTSPIPKARPEGRITWAQPGYPWPL 720
DB 661 NRRPDQVFPGGQIIVGGVILLPRRGLRLVLAATKTSPIPKARPEGRITWAQPGYPWPL 720
QY 721 YGNKDRSTGSKGKPGYPWPRKTRNRRNPQDVKFGGGQIVGGVILLPRRGLRLV 780
DB 721 YGNKDRSTGSKGKPGYPWPRKTRNRRNPQDVKFGGGQIVGGVILLPRRGLRLV 780
QY 781 ATRKTSPIPKARPEGRITWAQPGYPWPLVYGNKDRSTGSKGKPGYPW 829
DB 781 ATRKTSPIPKARPEGRITWAQPGYPWPLVYGNKDRSTGSKGKPGYPW 829
RESULT 2
ADC06769
ID ADC06769 standard; protein; 829 AA.
XX
AC ADC06769;

XX 18-DEC-2003 (first entry)
DT Chimeric multiple epitope fusion antigen 12 protein.
DE immunoassay solid support; HCV; NS3/4a; non-structural;
XX non-A, non-B hepatitis; NANB; multiple epitope fusion antigen 12; MEFA12;
KW chimeric.
XX Chimeric.
OS Synthetic.
OS Unidentified.
OS Hepatitis C virus.
XX Homo sapiens.
EN US2002192639-A1.
XX 19-DEC-2002.
XX 14-JUN-2001; 2001US-00881239.
XX 15-JUN-2000; 2000US-0212082P.
PR 02-APR-2001; 2001US-0280811P.
PR 02-APR-2001; 2001US-0280867P.
XX (CHIE/) CHIEN D Y.
PA (ARCA/) ARCANGEL P.
PA (TAND/) TANDESKE L.
PA (GEOR/) GEORGE-NASCIMENTO C.
PA (COIT/) COIT D.
PA (MEDI/) MEDINA-SELBY A.
XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
PI Medina-Selby A;
XX WPI; 2003-644609/61.
DR N-PSDB; ADC06770.
XX Immunassay solid support for detecting hepatitis C virus infection in
PT biological samples, comprises a hepatitis C virus anti-core antibody and
PT an isolated hepatitis C virus NS3/4a epitope bound HCV anti-core
XX antibody.
PS Claim 45; Fig 7; 40pp; English.
XX The invention relates to a novel immunoassay solid support comprising at
CC least one hepatitis C virus (HCV) anti-core antibody and at least one
CC isolated HCV NS3/4a (non-structural protein 3/4a) epitope bound thereto.
CC The system of the invention may be useful for detecting HCV infection in
CC a biological sample and for treating or detecting non-A, non-B hepatitis
CC (NANB hepatitis). The current sequence is that of the chimeric multiple
XX epitope fusion antigen 12 (MEFA12) protein of the invention.
XX Sequence 829 AA;
SQ
Query Match 100.0%; Score 4455; DB 7; Length 829;
Best Local Similarity 100.0%; Pred. No. 1.7e-310;
Matches 829; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATKAVCVLKGDGPVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
DB 1 MATKAVCVLKGDGPVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
QY 61 AGPHFNPLSTRGCNCSIYPGHITGHRMAWKLGSAAARTTSGFVSLFAPGAKQNETHVTTGGA 120
DB 61 AGPHFNPLSTRGCNCSIYPGHITGHRMAWKLGSAAARTTSGFVSLFAPGAKQNETHVTTGGA 120
QY 121 AARTTSGLTSLFSPGASONIQLITSDNNSPPVQSFQVAHLHAPTGSKSTKVPAAAYA 180
DB 121 AARTTSGLTSLFSPGASONIQLITSDNNSPPVQSFQVAHLHAPTGSKSTKVPAAAYA 180
QY 181 AAGYKVLVLPNSVAATLGFAGYMSKAHGIDPNIRITGVRTITITGSPITYSTYKFLADGGC 240

Db 181 AQQYKVLNPNVAATLGFAYMSKAHGIDPNIRTCVRIITGSPITYSTYKFLADGGC 240
 QY 241 SGGAYDIIICDECHSTDATSIILGIGTVLDQAEAGARLVVLTATATPPGVSIVPHNIEV 300
 Db 241 SGGAYDIIICDECHSTDATSIILGIGTVLDQAEAGARLVVLTATATPPGVSIVPHNIEV 300
 QY 301 ALSTTGEIPFYGKAPLEVIKGRHLIFCHSKKKCDLAALVALGINAVAYRGLDVS 360
 Db 301 ALSTTGEIPFYGKAPLEVIKGRHLIFCHSKKKCDLAALVALGINAVAYRGLDVS 360
 QY 361 IPTSGDVVVVATDALMTGVTGDFSDVIDCNTCAGSKGPAIIPDREVLVREFDEMECSOH 420
 Db 361 IPTSGDVVVVATDALMTGVTGDFSDVIDCNTCAGSKGPAIIPDREVLVREFDEMECSOH 420
 QY 421 LPYIEQGMMLAQFKOKALGLSRGKPAIVPKVLYQOYDEMECSQAAPYIEQAQVIA 480
 Db 421 LPYIEQGMMLAQFKOKALGLSRGKPAIVPKVLYQOYDEMECSQAAPYIEQAQVIA 480
 QY 481 HOFKEKVLGLINDQVVVTPDKELLYEAFDEMECSKAAALTEBQORMAEMLKSKIQLL 540
 Db 481 HOFKEKVLGLINDQVVVTPDKELLYEAFDEMECSKAAALTEBQORMAEMLKSKIQLL 540
 QY 541 GILRHVHGEGAVQWNNRLIAPASRGNEHVSPTHYVPSRRRFAQALPVWARPDPNPLV 600
 Db 541 GILRHVHGEGAVQWNNRLIAPASRGNEHVSPTHYVPSRRRFAQALPVWARPDPNPLV 600
 QY 601 ETWKKPDYPPVHVGSSRRRFAQALPVWARPDPNPLVETWKKPDYPPVHVGRTKRT 660
 Db 601 ETWKKPDYPPVHVGSSRRRFAQALPVWARPDPNPLVETWKKPDYPPVHVGRTKRT 660
 QY 661 NRRPDVFPGGQIVGGVYLLPRGPRGLVLTAKTSIPKARPEGTWQPGYPWEL 720
 Db 661 NRRPDVFPGGQIVGGVYLLPRGPRGLVLTAKTSIPKARPEGTWQPGYPWEL 720
 QY 721 YGNKDRRSTGKSGKPGYPPWPKRTKRTNRRPQDVKFGGQIVGGVYLLPRGPRGLV 780
 Db 721 YGNKDRRSTGKSGKPGYPPWPKRTKRTNRRPQDVKFGGQIVGGVYLLPRGPRGLV 780
 QY 781 ATRKTSPTPKARRPEGTWQPGYPPWPLYGNKDRRSTGKSGKPGYPPW 829
 Db 781 ATRKTSPTPKARRPEGTWQPGYPPWPLYGNKDRRSTGKSGKPGYPPW 829
 RESULT 3
 AAU76378
 ID AAU76378 standard; protein; 1099 AA.
 XX AC AAU76378;
 XX DT 08-MAY-2002 (first entry)
 XX DE HCV multiple epitope fusion antigen (MEFA) 7.1 protein sequence.
 XX KW Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;
 KW immunosassay solid support; multiple epitope fusion antigen; MEFA;
 KW non-structural protein.
 XX OS Hepatitis C virus.
 OS Synthetic.
 XX PN WO200196870-A2.
 XX PD 20-DEC-2001.
 XX 14-JUN-2001; 2001WO-US019156.
 XX 15-JUN-2000; 2000US-0212082P.
 PR 02-APR-2001; 2001US-0280811P.
 PR 02-APR-2001; 2001US-0280867P.
 XX (CHIR) CHIRON CORP.
 PA Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
 XX

PI Medina-Selby A;
 XX WPI; 2002-090228/12.
 DR N-PSDB; ABX15345.
 XX Immunoassay solid support, useful for detecting hepatitis C virus
 PT infection in biological sample, comprises HCV NS3/4a conformational
 PT epitope and multiple epitope fusion antigen bound to the support.
 XX Claim 5; Fig 5; 92pp; English.
 XX The present invention relates to a new immunoassay solid support
 CC consisting essentially of at least one hepatitis C virus (HCV) NS3/4a
 CC conformational epitope and a multiple epitope fusion antigen (MEFA),
 CC bound to the support. The NS3/4a conformational epitope and/or MEFA,
 CC reacts specifically with anti-HCV antibodies present in a biological
 CC sample from an HCV-infected individual. The immunoassay of the invention
 CC is useful for detecting hepatitis C virus infection in a biological
 CC sample. The method of the invention provides a sensitive, accurate
 CC diagnostic and prognostic tool to provide adequate patient care and to
 CC prevent transmission of HCV by blood and by blood products, or by
 CC personal contact. Use of NS3/4a conformational epitope in combination
 CC with MEFA, provides a sensitive and reliable method for detecting early
 CC HCV seroconversion. Use of MEFA has the added advantages of decreasing
 CC masking problems, improving sensitivity in detecting antibodies by
 CC allowing a greater number of epitopes on a unit surface area of
 CC substrate, and improving substrate. Detection accuracy is increased and
 CC the incidence of false results is reduced because of the identification
 CC and the use of highly immunogenic HCV antigens which are present during
 CC the early stages of HCV seroconversion. The present amino acid sequence
 CC represents the multiple epitope fusion antigen (MEFA) 7.1 of the
 CC invention
 XX
 SQ Sequence 1099 AA;
 Query Match 90.5%; Score 4032; DB 5; Length 1099;
 Best Local Similarity 69.8%; Pred. No. 5.4e-280;
 Matches 791; Conservative 1; Mismatches 3; Indels 338; Gaps 7;
 QY 1 MATKAVCVLKGDPVQGIINFEQESNGFVKVWSIKGLTEGLHGFHVEFGDNTAGCTS 60
 Db 1 MATKAVCVLKGDPVQGIINFEQESNGFVKVWSIKGLTEGLHGFHVEFGDNTAGCTS 60
 QY 61 AGPHENPLSTR----- 71
 Db 61 AGPHENPLSRKHGPKDBERHVGDLGNVTADKGVADVSIEDSVLSGDHCIIGRTLIV 120
 QY 72 -----GCNCSIYFGHITGHRMAWKLS 93
 Db 121 HEKADDLKGGNESTKYNAGSRLACGVIGIAQNLNSGCNCSIYFGHITGHRMAWKLS 180
 QY 94 AARTTSGFVSLFAPGAKQNETHTVGTGAARTTSGTSLFSPGASQNIQLITS----- 145
 Db 181 AARTTSGFVSLFAPGAKQNETHTVGTGAARTTSGTSLFSPGASQNIQLIVDFIPVENLE 240
 QY 146 -----TDNSSPPVFPQSOVAHLHAPTGSCKTKVPAAYAAQYKVLNPNVAATL 197
 Db 241 TTMRSPVFTDNSSPPVFPQSOVAHLHAPTGSCKTKVPAAYAAQYKVLNPNVAATL 300
 QY 198 GFGAYMSKAHGIDPNIRTCVRIITGSPITYSTYKFLADGGCSGGAYDIIICDECHSTD 257
 Db 301 GFGAYMSKAHGIDPNIRTCVRIITGSPITYSTYKFLADGGCSGGAYDIIICDECHSTD 360
 QY 258 ATSLIGIGTVLDQAEAGARLVVLTATATPPGVSIVPHNIEVALSTTGEIPFYGKAIP 317
 Db 361 ATSLIGIGTVLDQAEAGARLVVLTATATPPGVSIVPHNIEVALSTTGEIPFYGKAIP 420
 QY 318 EVIKGGRHLIFCHSKKKCDLAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALMT 377
 Db 421 EVIKGGRHLIFCHSKKKCDLAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALMT 480
 QY 378 GYTGDFDSVIDCNTC----- 392

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Db 481 GYTGDFDSVIDNCTVQTQTVDFSLDPTFTIITLPQDAVSRTQRRGRTGKGPYIRFV 540
Qy 393 -----
Db 541 APGERPSGMFDSVLCYDAGCAWYELTTPAETTVRLRAYMNTPLPVCQDHLFMEGVF 600
Qy 393 -----
Db 601 TGLTHIDAHFLSQTKQSGENLPYLVAQVVCARAQAPPSSDQWQKCLIRLKLTLHGPT 660
Qy 393 -----
Db 661 PLLVRLGAVQNEITLTHPTVKYIMTCMSADLEVVTSSACSGKPAIIPDREVLYRFEDEME 720
Qy 417 CSQHLPIYIEQGMMLAEQFKQKALGSRGGKPAIVDPKVELYQOYDEMECSQAAPYIEQA 476
Db 721 CSQHLPIYIEQGMMLAEQFKQKALGSRGGKPAIVDPKVELYQOYDEMECSQAAPYIEQA 780
Qy 477 QVIAHQKFKVLGLINDQVVVTPDKELLYEAFDEMEECASKAALIEEGQSMAEMLKSKI 536
Db 781 QVIAHQKFKVLGLINDQVVVTPDKELLYEAFDEMEECASKAALIEEGQSMAEMLKSKI 840
Qy 537 QGLLGILRRHVGPGEQAVQWNNRLIAPASRGNHVSPHYVPSRRFAQALPVMWARDYN 596
Db 841 QGLLGILRRHVGPGEQAVQWNNRLIAPASRGNHVSPHYVPSRRFAQALPVMWARDYN 900
Qy 597 PPLVETWKKDPYRPPVHGSSRRFAQALPVMWARDYNPPLVETWKKDPYRPPVHGSKT 656
Db 901 PPLVETWKKDPYRPPVHGSSRRFAQALPVMWARDYNPPLVETWKKDPYRPPVHGSKT 960
Qy 657 KRNTNRPPQDVKPPGGQIVGGVLLPRGPRGLGLATKTSPIPKARRPGRRTWAQPGY 716
Db 961 KRNTNRPPQDVKPPGGQIVG-----RRGP-----PIPKARRPGRRTWAQPGY 1003
Qy 717 PWPLYGNKDRRSTCKSGKPGYPWPRKTKRNTNRPPQDVKPPGGQIVGGVLLPRGRPR 776
Db 1004 PWPLYGNKDRRSTCKSGKPGYPWPRKTKRNTNRPPQDVKPPGGQIVG-----RRGP- 1056
Qy 777 LGVLATKTSPIPKARPEGRRTWAQPGYPWPLYGNKDRRSTCKSGKPGYPWP 829
Db 1057 -----PIPKARPEGRRTWAQPGYPWPLYGNKDRRSTCKSGKPGYPWP 1099

RESULT 4
ID ABG72262 standard; protein; 1099 AA.
XX AC ABG72262;
XX DT 06-MAR-2003 (first entry)
XX DE HCV multiple epitope fusion antigen 7.1 (MEFA 7.1).
XX KW Immunoassay solid support; Hepatitis C Virus type-1; HCV-1; HCV-2;
KW NS3/4a conformational epitope; multiple epitope fusion antigen 7.1;
KW MEFA 7.1; anti-HCV antibody; NS3/4a conformational antigen; HCV-3;
KW HCV infection; Hepatitis C Virus type-2; Hepatitis C Virus type-3;
KW mutant; mutain.
XX OS Hepatitis C virus type 1.
OS Hepatitis C virus type 2.
OS Hepatitis C virus type 3.
OS Synthetic.
OS Chimeric.
FH Key Location/Qualifiers
FT Region 1. .156
FT /note= "Correspond to amino acids 1-156 of HCV-1 NSOD
FT superoxide dismutase")
FT Region 159..176
FT /note= "Correspond to amino acids 303-320 of HCV-1 E1"
FT Region 179..199
FT /note= "Correspond to consensus sequence of amino acids
FT

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FT 390-410 of HCV-1 E2 HVR"
FT 200..230
FT /note= "Correspond to consensus sequence of amino acids
FT 384-414 of HCV-1 and HCV-2 E2 HVR"
FT 231..696
FT /note= "Correspond to amino
FT acids 1193-1658 of HCV-1
FT helicasae"
FT 699..745
FT /note= "Correspond to amino
FT acids 1689-1735 of HCV-1 5-1-
FT 1 epitope"
FT 748..794
FT /note= "Correspond to amino
FT acids 1689-1735 of HCV-3 5-1-
FT 1 epitope"
FT 797..843
FT /note= "Correspond to amino
FT acids 1689-1735 of HCV-2 5-1-
FT 1 epitope"
FT 846..881
FT /note= "Correspond to amino
FT polypeptide C100"
FT 884..919
FT /note= "Correspond to amino
FT acids 2278-2313 of HCV-1 NS5
FT region"
FT 922..957
FT /note= "Correspond to amino
FT acids 2278-2313 of HCV-1 NS5
FT region"
FT 958..1028
FT /note= "Correspond to core region antigenic determinants
FT from amino acids 9-32, 39-42 and 64-88 of HCV-1 and amino
FT acids 67-84 of HCV-2"
FT 1029..1099
FT /note= "Correspond to core region antigenic determinants
FT from amino acids 9-32, 39-42 and 64-88 of HCV-1 and amino
FT acids 67-84 of HCV-2"
XX US2002146685-A1.
XX 10-OCT-2002.
XX 14-JUN-2001; 2001US-00881654.
XX 15-JUN-2000; 2000US-0212082P.
XX 02-APR-2001; 2001US-0280811P.
XX 02-APR-2001; 2001US-0280867P.
XX (CHIE//) CHIEN D Y.
XX (ARCA//) ARCANGEL P.
XX (TAND//) TANDESKE L.
XX (GEOR//) GEORGE-NASCIMENTO C.
XX (COIT//) COIT D.
XX (MEDI//) MEDINA-SELBY A.
XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
XX Medina-Selby A;
XX WPI; 2003-147573/14.
XX N-PSDB; ABX14411.
XX Immunoassay solid support for detecting Hepatitis C Virus infection in
XX biological samples, comprises Hepatitis C Virus conformational epitope
XX and multiple epitope fusion antigen.
XX Claim 25; Fig 5A-5F; 45pp; English.
XX The present invention relates to immunoassays comprising Hepatitis C
XX virus (HCV) NS3/4a conformational epitope and multiple epitope fusion
XX antigen (MEFA), bound to a solid support. The NS3/4a epitope and/or the
XX multiple epitope fusion antigen react with anti-HCV antibodies present in
XX a biological sample from an HCV-infected individual. The immunoassays and
XX methods of the invention are useful for detecting HCV infection in a
XX biological sample. The inventive immunoassay solid support provides a
XX sensitive and reliable method for detecting early HCV seroconversion. The
XX assays can detect HCV infection caused by any six known genotypes of HCV.
XX The use of the multiple epitope fusion proteins decreases masking

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CC problems, improves sensitivity in detecting antibodies by allowing a
CC greater number of epitopes on a unit area of substrate, and improves
CC selectivity. The present sequence represents HCV multiple epitope fusion
CC antigen 7.1 (MEFA 7.1), a mutant HCV polypeptide derived from various
CC regions of HCV type 1, 2, or 3 (HCV-1, HCV-2, or HCV-3) polypeptide
CC sequences
XX
SQ Sequence 1099 AA;
Query Match 90.5%; Score 4032; DB 6; Length 1099;
Best Local Similarity 69.8%; Pred. No. 5.4e-280;
Matches 791; Conservative 1; Mismatches 3; Indels 338; Gaps 7;
QY 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLHGHVHFEFGDNTAGCTS 60
Db 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLHGHVHFEFGDNTAGCTS 60
QY 61 AGPHENPLSTR----- 71
Db 61 AGPHENPLSRKHGGPKDEHRHVDLGNVTADKGVADVSIEDSVISLSDGHCIIIGRTLTV 120
QY 72 -----GCNGSIYPGHITGHRMAWKLS 93
Db 121 HEKADDLGKGGNEESTKTGNAGSLACGVIGIAQNLSGNCNSIYFGHITGHRMAWKLS 180
QY 94 AARTSGFVSLPAPGAKQNEHTVGTGAARTTSGLTSLFSPGASONIQLITS----- 145
Db 181 AARTTSGFVSLPAPGAKQNEHTVGTGAARTTSGLTSLFSPGASONIQLIVDFIPVENLE 240
QY 146 -----TDNSSPPVPPQSFQVAHLHAPTGSKSTKVPAAAYAAQYKVLVLPNSVAATL 197
Db 241 TTMRSPTDSSPPVPPQSFQVAHLHAPTGSKSTKVPAAAYAAQYKVLVLPNSVAATL 300
QY 198 GFGYMSKAHGIDPNIRTVRTITGSPITYTYGKFLADGCGSGAYDIILICDECHSTD 257
Db 301 GFGYMSKAHGIDPNIRTVRTITGSPITYTYGKFLADGCGSGAYDIILICDECHSTD 360
QY 258 ATSILGIGTVLDOETAGARLVVLTATPPGVTVPHPNIEVALSTTGEIIFYKAIPL 317
Db 361 ATSILGIGTVLDOETAGARLVVLTATPPGVTVPHPNIEVALSTTGEIIFYKAIPL 420
QY 318 EVIKGRHLIFCHSKKKDELAALVGINAVAYRGDVSIVPTSGDVVVVATDALMT 377
Db 421 EVIKGRHLIFCHSKKKDELAALVGINAVAYRGDVSIVPTSGDVVVVATDALMT 480
QY 378 GYTGFDSVIDNCTC----- 392
Db 481 GYTGFDSVIDNCTCTQTQVDFSLDPTFTTITLTPQDAVSRTQRRGTGRGKGIYRFV 540
QY 393 ----- 392
Db 541 AFGERPFGMFDSSVLCECYDAGCAMEYELPAETTVLRAYMNTPLGPLVCQDHLFEWGVF 600
QY 393 ----- 392
Db 601 TGLTHIDAHFLSQTQKSGENLPLVAYQATVCARAQAPPPSDQWKKLIRLKPILHGT 660
QY 393 -----ACSGKPAIIPDREVLYREFDEME 416
Db 661 PLLYRLGAVONEITLTHPVTKVIMTCSADLEWVTSACSGKPAIIPDREVLYREFDEME 720
QY 417 CSCHLPYIEQGMMLARQFKQKALGLSRGKPAIVDPKVELVYQYDMECSQAAPYIEQA 476
Db 721 CSCHLPYIEQGMMLARQFKQKALGLSRGKPAIVDPKVELVYQYDMECSQAAPYIEQA 780
QY 477 QVIAHQFKEKVLGLINDQVVTTPDKEILYEAFDEMEECASKAALIEEGORMAELMSKI 536
Db 781 QVIAHQFKEKVLGLINDQVVTTPDKEILYEAFDEMEECASKAALIEEGORMAELMSKI 840
QY 537 QGLGLILRRHVGEGAGVQMMNRLIAFASRGNHVSPTHYVPSRRRFAQALPVPWAPDYN 596
Db 841 QGLGLILRRHVGEGAGVQMMNRLIAFASRGNHVSPTHYVPSRRRFAQALPVPWAPDYN 900

QY 597 PPLVETWKKPDYEPVPHGRSRRRFAQALPVPWAPDYNPPLVETWKKPDYEPVPHGRKT 656
Db 901 PPLVETWKKPDYEPVPHGRSRRRFAQALPVPWAPDYNPPLVETWKKPDYEPVPHGRKT 960
QY 657 KRNTRRRPQDVKFGGQIIVGGVLLPRRGRELGLVLAIRKTSPIPKARRPEGRRTWAQPGY 716
Db 961 KRNTRRRPQDVKFGGQIIVGGVLLPRRGRELGLVLAIRKTSPIPKARRPEGRRTWAQPGY 1003
QY 717 PMPLYGNKDRRSTGKSGKPGYPWPWKTKRNTNRRPQDVKFGGQIIVGGVLLPRRGPR 776
Db 1004 PMPLYGNKDRRSTGKSGKPGYPWPWKTKRNTNRRPQDVKFGGQIIVGGVLLPRRGPR 1056
QY 777 LGVLATKTSPIPKARRPEGRRTWAQPGYPWPPLYGNKDRRSTGKSGKPGYPWP 829
Db 1057 -----PIPKARRPEGRRTWAQPGYPWPPLYGNKDRRSTGKSGKPGYPWP 1099
RESULT 5
AAW34481
ID AAW34481 standard; protein; 1021 AA.
XX
AC AAW34481;
XX
DT 25-MAR-2003 (revised)
DT 16-MAR-1998 (first entry)
XX
DE HCV antigen combination pSOD/c200/core.
XX
KW PCR primer; amplify; HCV; hepatitis C virus; antigen combination; NS3;
KW C domain; S domain; NS5; HCV polypeptide; anti-HCV antibody; detection;
KW NS4.
OS Hepatitis C virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..902 /note="linker"
FT Misc-difference 1..154 /note="hsod fragment"
FT Misc-difference 155..159 /note="linker"
FT Misc-difference 160..899 /note="c200 (amino acids 1192-1931 of HCV polypeptide)"
FT Misc-difference 903..1021 /note="c22 (amino acids 2-120 of HCV polypeptide)"
XX
XX US5683864-A.
XX
XX 04-NOV-1997.
XX
XX 07-JUL-1992; 92US-00910760.
XX
XX 18-NOV-1987; 87US-00122714.
XX 30-DEC-1987; 87US-00139886.
XX 26-FEB-1988; 88US-00161072.
XX 06-MAY-1988; 88US-00191263.
XX 26-OCT-1988; 88US-00263584.
XX 14-NOV-1988; 88US-00271450.
XX 17-MAR-1989; 89US-00325338.
XX 20-APR-1989; 89US-00341334.
XX 21-APR-1989; 89US-00353896.
XX 18-MAY-1989; 89US-00355002.
XX 04-APR-1990; 90US-00504352.
XX (CHIR) CHIRON CORP.
XX
XX Kuo G, Houghton M, Choo Q;
XX
XX WPI; 1997-548976/50.
XX DR N-PSDB; AAT99982.
XX
XX Combination of three hepatitis C virus antigens - used for detection of

PT specific antibodies to diagnose infection.
XX Example 6; Col 59-68; 57pp; English.
XX This sequence represents a Hepatitis c virus (HCV) antigen combination of
CC the invention. The HCV antigen combination comprises an antigen (Ag1)
CC comprising the C domain (i.e. amino acids (aa) 1-120 of the HCV
CC polyprotein), or its immunologically reactive fragment containing at
CC least 8 aa. It also comprises two additional antigens from two different
CC polyprotein domains, including at least 8 aa from the NS3, NS4, S or NS5
CC domains of the polyprotein, corresponding, respectively, to aa 1050-1640;
CC 1640-2000; 120-400 and 2000-3011 of the HCV polyprotein. Alternatively,
CC Ag1 contains at least 8 aa from the 1-122 or 9-177 aa regions of the HCV
CC polyprotein. These antigen combinations are used diagnostically to detect
CC anti-HCV antibodies, using any standard immunoassay format. These antigen
CC combinations have a broader range of reactivity with antibodies than any
CC antigen individually. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 1021 AA;
Query Match 49.9%; Score 2222; DB 2; Length 1021;
Best Local Similarity 46.2%; Pred. No. 3e-150;
Matches 512; Conservative 35; Mismatches 111; Indels 450; Gaps 22;
QY 1 MATKAVCVLKGDPVQGIINFEQKESGPKVWGSIKGLTEGLHGFHVEFGDNTAGCTS 60
DB 1 MATKAVCVLKGDPVQGIINFEQKESGPKVWGSIKGLTEGLHGFHVEFGDNTAGCTS 60
QY 61 AGPHNPLSTRGCNCSYPGHITGHRMAWLKGSARTTSQ-----FVSL----- 104
DB 61 AGPHNPLSRK-----HGPKDEERHVGDLGNVADKGVADVSIEDSVLSGDHCII 114
QY 105 -----FAPGAKQNEHTVTGGAARTTSGLTSLFSPGASQNIQ----- 141
DB 115 GRTLVHEKADDLKGKGNESBK-TGNAGSLACGVI-----GIAQNLDFGAVDFIPVEN 168
QY 142 LIITS-----TDNSSPPVPOFVAHLHAPTGSKSTKPEAAQAQYKVLNPSVAA 195
DB 169 LETTMRSPVFTDNSSPPVPOFVAHLHAPTGSKSTKPEAAQAQYKVLNPSVAA 228
QY 196 TLGFGAYMSKAHGDIPNIRTVRTTGSPTTSTYKFLADGGCSGAYDIIICDECHS 255
DB 229 TLGFGAYMSKAHGDIPNIRTVRTTGSPTTSTYKFLADGGCSGAYDIIICDECHS 288
QY 256 TDATSIIGIGVLDQAEATAGARLVLTATPPGVTVPHPNIEVALSTTGEIPFYGKAI 315
DB 289 TDATSIIGIGVLDQAEATAGARLVLTATPPGVTVPHPNIEVALSTTGEIPFYGKAI 348
QY 316 PLEVIKGRHLIFCHSKKKCDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDAL 375
DB 349 PLEVIKGRHLIFCHSKKKCDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDAL 408
QY 376 MTGYTGDFDSVIDCNC----- 392
DB 409 MTGYTGDFDSVIDCNCVTQTVDLPTFTTITLTPQDAVSTQRGRGTGRGKPGIYR 468
QY 393 ----- 392
DB 469 FVAPGERPSGDFSSVLCEDACANWELTPAETTVRLRAYMNTPGIPVQCDHLEFWEG 526
QY 393 ----- 392
DB 529 VFTGLTHIDAHFLSGTKSGENLPVLVAYQATVCARAQAPPPSWDQWKKLRLKPTLHG 588
QY 393 ----- 392
DB 589 PTLPLLYLGAQVQNEITHTPVTKYIMTCMSADLEVTSTWLVGGVLAALAAAYCLSTGCV 648
QY 393 -----ACSGKPAIPDREVLRYRFDENECQSQHLPTIEQGMMLAEQFKQALGL-----S 442
DB 649 VIVGRVLSGKPAIPDREVLRYRFDENECQSQHLPTIEQGMMLAEQFKQALGLQTAS 708
QY 443 RGGKPAIVDPKEVLYQQYD-----EMECSSQAAPYIEQAQVIAHQFKEKVLGLIDNQV 497

Db 709 ROAE-VIAPAVQTNQXLETFWAKHMNFISGIOYLAGLSTLPG--NPALIASLMAFTAAV 765
QY 498 VTP---DKELIYE-----AFDEMEBCASKAALIEGQORVAEMLKSKIQ 537
Db 766 TSPLTTSTQTLLENLILGWVAAQLAAPGAATAFVAGLAGAIGSVGLGKVLIDILAGYGA 825
QY 538 GLILG-----ILRRHVGPGEAGAVOMN 558
Db 826 GVAGALVAFKIMSGEVSTEDLVNLLPAILSPGALVGVVCAAILRRHVGEAGAVOMN 885
QY 559 RLIAFASGRGHVSPHYVPSRSRFAQALPVMAREPDYNPPLVETWKKPDYPPVHVGRSS 618
Db 886 RLIAFASGRGHVSP-----GNSS 903
QY 619 RRFQAALPVWARPDPYNPPLVETWKKPDYPPVHVGRKTKRNTNRRPQDVKPPGGQIVGG 678
Db 904 T-----NP-----KPO-----KKNKNTNRRPQDVKPPGGQIVGG 934
QY 679 VYLLPRGPRGLVLAIRKTS-----PIPKARPEGRTPAQPGYPWPPLYGNK----- 724
Db 935 VYLLPRGPRGLVLAIRKTSERSQPRGRQPIPKARPEGRTPAQPGYPWPPLYGNEGCGW 994
QY 725 -----DRSTGKSGWKPGYPWPRTKEN 747
Db 995 AGWLLSPRGSRPSSWGPTD---PRRRSRN 1019

RESULT 6
AAW40039
ID AAW40039 standard; protein; 1021 AA.
XX AC AAW40039;
XX DT 26-MAY-1998 (first entry)
XX DE Fusion protein c200/c22.
XX KW Hepatitis C virus C domain; HCV; immunological activity; c200/c22;
XX NS3 domain; NS4 domain; S domain; NS5 domain; fusion protein.
XX OS Synthetic.
XX OS Hepatitis virus.
XX FN US5712087-A.
XX PD 27-JAN-1998.
XX PF 12-MAY-1995; 95US-00440519.
XX PR 04-APR-1990; 90US-00504352.
XX PR 07-JUL-1992; 92US-00910760.
XX (CHIR) CHIRON CORP.
XX Kuo G, Houghton M, Choo Q;
XX WPI; 1998-1159973/11.
XX N-PSDB; AAV09990.
XX Immunoassays for hepatitis C virus antibodies - using combinations of
XX antigenic fragments of HCV polyprotein.
XX Example 6; Fig 4; 59pp; English.
XX This sequence represents a fusion protein constructed from the hepatitis
XX C virus core domain (which is situated at the carboxy terminus of the
XX fusion protein) and a c200 construct (a fusion of the NS3 and NS3
XX domains). This protein used in the construction of novel combinations of
XX HCV antigens that have a broader range of immunological activity than any
XX single HCV antigen. An example of such an antigen given in this
XX specification comprises a first antigen containing at least 8 amino acids
XX of the C domain of the HCV polyprotein and a second antigen comprising at

CC Least 8 amino acids of the NS3 domain, the NS4 domain, the NS5 domain, the S domain or
CC the NS5 domain of the HCV polyprotein in the form of a fusion protein, a
CC physical mixture or bound to a solid matrix

XX Sequence 1021 AA;

Query Match 49.9%; Score 2222; DB 2; Length 1021;

Best Local Similarity 46.2%; Pred. No. 3e-150;

Matches 512; Conservative 35; Mismatches 111; Indels 450; Gaps 22;

QY 1 MATKAVCVLKGDPVQGIINFEKESNGPVKVGSIKGLTEGLGHFVHEFGDNTAGCTS 60

DB 1 MATKAVCVLKGDPVQGIINFEKESNGPVKVGSIKGLTEGLGHFVHEFGDNTAGCTS 60

QY 61 AGPHFNPLSTRGCNSIYPGHI:THGRMAWKLSAAARTTSG-----FVSL----- 104

DB 61 AGPHFNPLSRK-----HGGPKDEERHVGDLGNVTADKGDVSDIEDSVLSLGDHCHII 114

QY 105 -----FAPGAKQNETHTVGGAAARTTSGTSLFSPGASQNIQ----- 141

DB 115 GRTLNVHEKADDLGKGNNESTK-TGNAGSRLACGVI-----GIAQNLFGAVDFIPVEN 168

QY 142 LITS-----TNSSPVPVQSFQVAHLHAPTGSKSTKVPAAVAAQGVKVLVLPNSVAA 195

DB 169 LETTWESPVTDNSSPPVQSFQVAHLHAPTGSKSTKVPAAVAAQGVKVLVLPNSVAA 228

QY 196 TLGFGAYMSKAHGIDPNRTITTSPTIYSTYKFLADGCGSGGAYDIIICDECHS 255

DB 229 TLGFGAYMSKAHGIDPNRTITTSPTIYSTYKFLADGCGSGGAYDIIICDECHS 288

QY 256 TDATSLGHTGLVDOAETAGALVLAATPPGTVVPHNIEEVALSTTGEIPYFKAI 315

DB 289 TDATSLGHTGLVDOAETAGALVLAATPPGTVVPHNIEEVALSTTGEIPYFKAI 348

QY 316 PLEVTKGGRHLIFCHSKKCDLAALVAGLNAVAYRGLDVSVTPSGDVVVATDAL 375

DB 349 PLEVTKGGRHLIFCHSKKCDLAALVAGLNAVAYRGLDVSVTPSGDVVVATDAL 408

QY 376 MTGYTGDFSDVIDDNTC----- 392

DB 409 MTGYTGDFSDVIDDNTC----- 392

QY 393 ----- 392

DB 469 FVAPGERPSGMDSVLCEYDAGCAWYELTPAETTVRLRAYMTPGLPVCQDHLFEWEG 528

QY 393 ----- 392

DB 529 VFTGLTHIDAHFLSQTQSGENLPIYVAQATVCARAQAPPSPSDQMWKCLIRLPTLHG 588

QY 393 ----- 392

DB 589 PTPLLYRLGAVONEITLHPVTKYIMTCSADLEVVTSTWLVGVGLAALAAAYCLSTGCV 648

QY 393 -----ACSGKEPALTIDREVLRYEDEMEECSCHLPYIEQGMMLAEQFKQKALGL-----S 442

DB 649 VIVGAVVLSGKPAIIPDREVLRYEDEMEECSCHLPYIEQGMMLAEQFKQKALGLQTAS 708

QY 443 RGGKPAIVDPKEVLYQQVD-----EMEECSQAAPYIEQAQVIAHQFKEKVLGLINDQV 497

DB 709 RQAE-VIAPAVQTNQKLETFWAKHWNFIISQIYLAGLSTLPG--NPAIASLMAFTAAV 765

QY 498 VTP-----DKBILYE-----AFDEMEECASKAALIBEGQRMALMKSKITQ 537

DB 766 TSPLTATSTQLLENILGGWVAQAALAPGAATAFVAGLAGAAGTSGVGLGKVLIDILAGYGA 825

QY 538 GLLG-----ILRRHVGPGEQAVQWNN 558

DB 826 GVAGALVAFKIMSGEVPSTEDLVNLLPALSLPCALVGVVCAAILLRHVGPGEQAVQWNN 885

QY 559 RLIAFASRGNHVSPTHYVPSRRRFAQALPVNARPDYNPLVETWKKPDYEPVHVGRSS 618

DB 886 RLIAFASRGNHVSPTHYVPSRRRFAQALPVNARPDYNPLVETWKKPDYEPVHVGRSS 903

QY 619 RRAQALPVWARPDPNPLVETWKKPDYEPVHVGRKTKRNTNRRPQDVKFFGGQIVGG 678

DB 904 T-----NP-----KPKQ-----KKKRNNTNRRPQDVKFFGGQIVGG 934

QY 679 VYLLPRGRPLGLVLAATKTS-----PIPKARRPEGRTPAOPGYWPLVGNK----- 724

DB 935 VYLLPRGRPLGLVLAATKTS-----PIPKARRPEGRTPAOPGYWPLVGNK----- 994

QY 725 -----DRESTGKSGKPGVWPRKTKRN 747

DB 995 AGWLLSPGRSPSWGPTD-----PRRSRN 1019

RESULT 7

AAE22050

ID AAE22050 standard; protein; 1021 AA.

XX AAE22050;

DT 16-JUL-2002 (first entry)

XX pSOD/c200/core expression plasmid protein.

DE Hepatitis C virus; HCV; antigen; C domain; polyprotein; NS3 domain;

KW NS4 domain; S domain; NS5 domain; pSOD/c200/core plasmid.

XX Hepatitis C virus.

OS Unidentified.

OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..154

FT /note= "hsOD"

FT Region 155..159

FT /note= "Linker region"

FT Region 160..899

FT /note= "HCV c200"

FT Region 900..902

FT /note= "Linker region"

FT Region 903..1021

FT /note= "HCV c22"

XX US6312889-B1.

PN 06-NOV-2001.

PD 12-MAY-1995; 95US-00440549.

PF 04-APR-1990; 90US-00504352.

PR 07-JUL-1992; 92US-00910760.

XX (CHIR) CHIRON CORP.

XX Houghton M, Choo Q, Kuo G;

PI WPI; 2002-040268/05.

XX N-PSDB; AAD35044.

DR Combination of hepatitis C viral (HCV) antigens, useful in improved

XX immunoassay for detecting HCV antibodies.

PT Example 6; Fig 4; 58pp; English.

PS The invention relates to combination of hepatitis C viral (HCV) antigens

XX that have a broader range of immunological reactivity than any single HCV

CC antigen. The combinations consist of an antigen from the C domain of the

CC HCV polyprotein, and at least one additional HCV antigen from either the

CC NS3 domain, the NS4 domain, the NS5 domain, or the NS5 domain and are in

CC the form of fusion protein, a simple physical mixture, or the individual

CC antigens commonly bound to a solid matrix. The combinations of antigens

CC provides broad range immunoassays for anti-HCV antibodies. The invention

CC therefore provides a method for detecting antibodies to HCV in a mammal

CC suspected of containing such antibodies. The present sequence is a
CC protein encoded by pSOB/c200/core expression plasmid DNA containing HCV
CC coding sequence
XX
SQ Sequence 1021 AA;

Query Match 49.9%; Score 2222; DB 5; Length 1021;
Best Local Similarity 46.2%; Pred. No. 3e-150;
Matches 512; Conservative 35; Mismatches 111; Indels 450; Gaps 22;

QY 1 MATKAVCVLKGDPVQGIINFEQESNGSPVKWGSIKGLTEGLHGHVHEFGDNTAGCTS 60
DB 1 MATKAVCVLKGDPVQGIINFEQESNGSPVKWGSIKGLTEGLHGHVHEFGDNTAGCTS 60

QY 61 AGHFNPSTGNCNCTYPGHITGRMAWKLGSARTTSG-----FVSL----- 104
DB 61 AGHFNPSTGNCNCTYPGHITGRMAWKLGSARTTSG-----FVSL----- 104

QY 105 -----FAPGAKQETHVTGGAAARTTSGTSLFSPGASQNIQ----- 141
DB 105 -----FAPGAKQETHVTGGAAARTTSGTSLFSPGASQNIQ----- 141

QY 142 LITS-----TDNSSPPVPOSFOVAHILHPTGSGKSTKVPAAVAAQYKVLVNPVAA 195
DB 142 LITS-----TDNSSPPVPOSFOVAHILHPTGSGKSTKVPAAVAAQYKVLVNPVAA 195

QY 169 LETMRSPTVFTDNSSPPVPOSFOVAHILHPTGSGKSTKVPAAVAAQYKVLVNPVAA 228
DB 169 LETMRSPTVFTDNSSPPVPOSFOVAHILHPTGSGKSTKVPAAVAAQYKVLVNPVAA 228

QY 196 TLGFGAYMSKAGIDPNIRGTRITTSPTSTYTYGKFLADGGCGGAYDIIICDECHS 255
DB 196 TLGFGAYMSKAGIDPNIRGTRITTSPTSTYTYGKFLADGGCGGAYDIIICDECHS 255

QY 229 TLGFGAYMSKAGIDPNIRGTRITTSPTSTYTYGKFLADGGCGGAYDIIICDECHS 288
DB 229 TLGFGAYMSKAGIDPNIRGTRITTSPTSTYTYGKFLADGGCGGAYDIIICDECHS 288

QY 256 TDATSIILGIGTLDQAEATAGARLVVLTATPPGSGVTVPHPNIEEVALSTTGEIPFYGKAI 315
DB 256 TDATSIILGIGTLDQAEATAGARLVVLTATPPGSGVTVPHPNIEEVALSTTGEIPFYGKAI 315

QY 289 TDATSIILGIGTLDQAEATAGARLVVLTATPPGSGVTVPHPNIEEVALSTTGEIPFYGKAI 348
DB 289 TDATSIILGIGTLDQAEATAGARLVVLTATPPGSGVTVPHPNIEEVALSTTGEIPFYGKAI 348

QY 316 PLEVIGKGRHLIFCHSKKKCDELAALVALGINAVAYRGLDVSVIPTSGDVVVVATDAL 375
DB 316 PLEVIGKGRHLIFCHSKKKCDELAALVALGINAVAYRGLDVSVIPTSGDVVVVATDAL 375

QY 349 PLEVIGKGRHLIFCHSKKKCDELAALVALGINAVAYRGLDVSVIPTSGDVVVVATDAL 408
DB 349 PLEVIGKGRHLIFCHSKKKCDELAALVALGINAVAYRGLDVSVIPTSGDVVVVATDAL 408

QY 376 MTGVTGDFSDVIDNCTC----- 392
DB 376 MTGVTGDFSDVIDNCTC----- 392

QY 409 MTGVTGDFSDVIDNCTC----- 468
DB 409 MTGVTGDFSDVIDNCTC----- 468

QY 393 ----- 392
DB 393 ----- 392

QY 469 FVAPGERPSGDFSSVLCYDAGCAWVELTPAETTVLRAYMTPGLPVQCDHLEWEG 528
DB 469 FVAPGERPSGDFSSVLCYDAGCAWVELTPAETTVLRAYMTPGLPVQCDHLEWEG 528

QY 393 ----- 392
DB 393 ----- 392

QY 529 VFTGLTHIDAFHLSQTKSGENLPYVAYQATVCARAQAPPPSWDMWKILRLKPTLHG 588
DB 529 VFTGLTHIDAFHLSQTKSGENLPYVAYQATVCARAQAPPPSWDMWKILRLKPTLHG 588

QY 393 ----- 392
DB 393 ----- 392

QY 589 PTPLLYBLGAVQNEITLTHPVTKYIMTCMSADLEWTVTWLVGVLAALAAAYCLSTGCV 648
DB 589 PTPLLYBLGAVQNEITLTHPVTKYIMTCMSADLEWTVTWLVGVLAALAAAYCLSTGCV 648

QY 393 -----ACSGKPAIPPREVLYREFDEMECSOHLPIYEQGMMLAEQFKALGL-----S 442
DB 393 -----ACSGKPAIPPREVLYREFDEMECSOHLPIYEQGMMLAEQFKALGL-----S 442

QY 649 VIVGRVLSGKPAIPPREVLYREFDEMECSOHLPIYEQGMMLAEQFKALGLQTA 708
DB 649 VIVGRVLSGKPAIPPREVLYREFDEMECSOHLPIYEQGMMLAEQFKALGLQTA 708

QY 443 RGGKPAIPPOKEVLYQQYD-----EMEECSAAPIYEQAVIAHQFKEKVLGLDNDQVV 497
DB 443 RGGKPAIPPOKEVLYQQYD-----EMEECSAAPIYEQAVIAHQFKEKVLGLDNDQVV 497

QY 709 RQAE-VIAPAVQTNWQKLETFWAKHMWNFTISGIQYLAGLSTLPG--NPATIASLMAFTA 765
DB 709 RQAE-VIAPAVQTNWQKLETFWAKHMWNFTISGIQYLAGLSTLPG--NPATIASLMAFTA 765

QY 498 VTP-----DKEIIE-----AFDEMEECASKAALTEFGORMAEMLKSKI 537
DB 498 VTP-----DKEIIE-----AFDEMEECASKAALTEFGORMAEMLKSKI 537

QY 766 TSPLTTSTQTLLENLIGWVAAQLAAPGRATAFVAGLAGAAGSVGLGKVLIDILAGVGA 825
DB 766 TSPLTTSTQTLLENLIGWVAAQLAAPGRATAFVAGLAGAAGSVGLGKVLIDILAGVGA 825

QY 538 GLLG-----ILRHVGEGEAVQVMN 558
DB 538 GLLG-----ILRHVGEGEAVQVMN 558

QY 826 GVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGWCAAILRRHVGEGEAVQVMN 885
DB 826 GVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGWCAAILRRHVGEGEAVQVMN 885

QY 559 RLIAFASRGNHVSPTHVPSRSRFAQALPWARNPDYNPPLVETWKKPDYPPVHVGRSS 618
DB 559 RLIAFASRGNHVSPTHVPSRSRFAQALPWARNPDYNPPLVETWKKPDYPPVHVGRSS 618

QY 886 RLIAFASRGNHVSPTHVPSRSRFAQALPWARNPDYNPPLVETWKKPDYPPVHVGRSS 903
DB 886 RLIAFASRGNHVSPTHVPSRSRFAQALPWARNPDYNPPLVETWKKPDYPPVHVGRSS 903

QY 619 RRFAQALPVWARPDPYNPPLVETWKKPDYEPVHVHRTKRNTRRRPODVKFPGGQIVGG 678
DB 304 T-----NP-----KPO-----KKKRNTRRRPODVKFPGGQIVGG 934

QY 679 VYLLPRGPRGLVLAATKTS-----PIKARRPEGRWTAQPGVWPVLYGNK----- 724
DB 935 VYLLPRGPRGLVLAATKTS-----PIKARRPEGRWTAQPGVWPVLYGNK----- 724

QY 725 -----DRSTGKSWGKPGYWPRTKRN 747
DB 995 AGWLLSPRGRPSWGPTD---PRRSRN 1019

RESULT 8
AAP2041
ID AAP2041 standard; protein; 1766 AA.
XX
XX AAP2041;
AC
DT 25-MAR-2003 (revised)
DT 02-MAR-1990 (first entry)
XX
XX Hepatitis C virus (HCV) cDNA inserts in clones 14i, 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g and 39c.
DE
XX Hepatitis C virus (HCV); non-A, non-B hepatitis (HANEH).
KW
XX Hepatitis C virus.
OS
XX
PN EP318216-A.
XX
PD 31-MAY-1989.
XX
PF 18-NOV-1988; 88EP-00310922.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
XX
XX (CHIR) CHIRON CORP.
XX (CHIR) CHIRON CORP.
PA
XX Houghton M, Choo QL, Kuo G;
PI
XX WPI; 1989-159274/22.
DR N-PSDB; AAN92097.
XX
XX Purified hepatitis C virus - and associated nucleic acids and polypeptide(s).
PT
XX Claim 13; Fig 26-1, 26-2, 26-3, 26-4, 26-5, 26-6; 139pp; English.
XX
XX It is the sequence encoded in the open reading frame of hepatitis C virus cDNA inserts in clones 14i, m 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g and 39c. It is antigenic and could be used in immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A, non-B hepatitis. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 1766 AA;

Query Match 36.5%; Score 1627.5; DB 1; Length 1766;
Best Local Similarity 36.6%; Pred. No. 2.7e-107;
Matches 398; Conservative 26; Mismatches 81; Indels 581; Gaps 15;

QY 146 TDNSSPPVPOSFOVAHILHPTGSGKSTKVPAAVAAQYKVLVNPVAAATLFGAYMSK 205
DB 495 TDNSSPPVPOSFOVAHILHPTGSGKSTKVPAAVAAQYKVLVNPVAAATLFGAYMSK 554


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QY 206 AHGIDPNIRTVGRTITTTGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSILGIG 265
Db 555 AHGIDPNIRTVGRTITTTGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSILGIG 614
QY 266 TVLDQAGTAGARLVLAATATPGSVTVPHPNIEEVALSTTGELPFYKAIPLIEVKGGRH 325
Db 615 TVLDQAGTAGARLVLAATATPGSVTVPHPNIEEVALSTTGELPFYKAIPLIEVKGGRH 674
QY 326 LIFCHSKKCCDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTGYTGDFDS 385
Db 675 LIFCHSKKCCDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTGYTGDFDS 734
QY 386 VIDCNTC----- 392
Db 735 VIDCNTCVTQTVDFSLDPTFTTITLPODAVSRTOGRGRTGRKPGIYRFVAPGRPSG 794
QY 393 ----- 392
Db 795 MFDSSVLCYDEGCANWYELTPAETTVLRAYMNTFGLPVCQDHLFEWEGVETGLTHIDA 854
QY 393 ----- 392
Db 855 HFLSOTKQSGENLPYLIVAYQATVWARAQAPPSWDQMWKCLIRLXETLHGPTPLLYRLGA 914
QY 393 -----ACSG 396
Db 915 VQNEILTHPTVKYIMTMSADLEVVTVTWLVGGVLAALAAAYCLSTGCVWIVGRVVLGG 974
QY 397 KPAILPDREVLVREDEMEECQHLPIYIEQGMWLABQFKQKALG----SRGKPAIVPD 452
Db 975 KPAILPDREVLVREDEMEECQHLPIYIEQGMWLABQFKQKALGQLLQTSRQAE-VIAPA 1033
QY 453 KEVLYQQVD-----EMECQAAPYIEQAQVIAHOFKEKVLGLDNDQVVTTP---DKBI 504
Db 1034 VQTNWQKLETFWAKHWNFIQIYQVLAGLSTLPG--NPALIASIMAFPTAATVTSPLTTSQTL 1091
QY 505 LYE-----AFDEMEECASKAALIEEQGMABMLKSKIQGLLG----- 541
Db 1092 LFNILGGWVAOLAAPGAATAFVGAGLAGAAGISVGLGKVLIDILAGYGAGVAGALVAPK 1151
QY 542 -----ILRRHVGPGEAGVQVNMRLIAFASRN 568
Db 1152 IMSGEVPTEDLVNLLPAILSPGALVVGVCAILRRHVGPGEAGVQVNMRLIAFASRN 1211
QY 569 HVSPTHYVPS----- 578
Db 1212 HVSPTHYVPSDAAARVTAISSLTVTLRLRHQWISSECTPCSGSWLRDIWDWICBV 1271
QY 579 ----- 578
Db 1272 LSDFKTLKAKLMPOLPGIPFVSCQGYKGVWRVDPGIMHTRCHCGABITHGVKNGTMRIV 1331
QY 579 ----- 578
Db 1332 GPRTCNMMSGTFPINAYTTGCTPLPADNYTFALWRVSAEYVEIRQVPSPEFTLDG 1391
QY 579 -RSRRA-----QALPVWARPDI----- 595
Db 1392 VRLHRFAPPCKELLREEVSRVGLHEYPVGSOLPCEPEPDVAULTSMLTDPSHITAEAG 1451
QY 596 -----NPP-----LVET---WKK----- 605
Db 1452 RRLARGSPSPVASSASQLSAPLSKATCTANHDSFDAELIEANLLRMGMGNITRVESE 1511
QY 606 -----PDYEPVWHG-----RSSRFAQALPVWARPDPYNPLVETWKKPDYE 647
Db 1512 NKWILDSFDPLVAEDEDEISVPAELIKSRFAQALPVWARPDPYNPLVETWKKPDYE 1571
QY 648 PPVWHG 653
Db 1572 PPVWHG 1577
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RESULT 9
AAP90164
ID AAP90164 standard; protein; 2261 AA.
XX
AC AAP90164;
XX
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
DE Peptide encoded by composite hepatitis C virus cDNA.
XX
KW Hepatitis C virus; clone 12f; clone 15e; probe; vaccine.
XX
OS Pan troglodytes.
XX
PN GB2212511-A.
XX
PD 26-JUL-1989.
XX
PF 18-NOV-1988; 88GB-00027024.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 26-OCT-1988; 88US-00263584.
XX
PA (CHIR ) CHIRON CORP.
XX
Houghton M, Choo QL, Kuo G;
XX
WPI; 1989-215054/30.
DR N-PSDB; AAN90331.
XX
Hepatitis C virus gene - used for prodn. of polynucleotide probes
PT polypeptide(s) and antibodies for diagnosis, prevention and treatment of
PT infection.
XX
PS Disclosure; Fig 32; 30pp; English.
XX
The sequence is the peptide encoded by the composite hepatitis C virus
CC (HCV) cDNA of AAN90331. The polypeptides are used to diagnose HCV-induced
CC NANBH, to raise antibodies for immunoassay or treatment, or to produce
CC vaccines. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 2261 AA;
Query Match 36.5%; Score 1624.5; DB 1; Length 2261;
Best Local Similarity 36.1%; Pred. No. 6.2e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;
QY 146 TDNSPPVPPVPSQFVAHLHAPTSGSKSTKVPAAAYAAQGYKVLNPNPSVAATLGFAYMSK 205
Db 586 TDNSPPVPPVPSQFVAHLHAPTSGSKSTKVPAAAYAAQGYKVLNPNPSVAATLGFAYMSK 645
QY 206 AHGIDPNIRTVGRTITTTGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSILGIG 265
Db 646 AHGIDPNIRTVGRTITTTGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSILGIG 705
QY 266 TVLDQAGTAGARLVLAATATPGSVTVPHPNIEEVALSTTGELPFYKAIPLIEVKGGRH 325
Db 706 TVLDQAGTAGARLVLAATATPGSVTVPHPNIEEVALSTTGELPFYKAIPLIEVKGGRH 765
QY 326 LIFCHSKKCCDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTGYTGDFDS 385
Db 766 LIFCHSKKCCDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTGYTGDFDS 825
QY 386 VIDCNTC----- 392
Db 826 VIDCNTCVTQTVDFSLDPTFTTITLPODAVSRTOGRGRTGRKPGIYRFVAPGRPSG 885
QY 393 ----- 392
```

Db 886 MFDSSVLCECYDAGCAWVELTPAETTVRLRAYMNTPLGVQCQHLEFWEFVFTGLTHIDA 945
QY 393 ----- 392
Db 946 HFLSQTQSGENLPYLVAQATVCARAQPPSWDMQMKLIRLKTPLHGTPLLYRLGA 1005
QY 393 -----ACSG 396
Db 1006 VQNEITLTHPVTKYIMTMSADLEVTSTWLVGVLAALAAAYCLSTGCVVIGRVLSG 1065
QY 397 KPAIIPREVLYRFBDEMECSQHLPYIEQGMMLAEQFKQKALGL-----SRGKPAIVPD 452
Db 1066 KPAIIPREVLYRFBDEMECSQHLPYIEQGMMLAEQFKQKALGLQATASQAE-VIAPA 1124
QY 453 KEVLYQQYD-----EMECSSAAPIEQAOVIAHQFKEKVLGLDNDQVVTTP--DKEI 504
Db 1125 VQTNWQKLETFWAKHMMNFISGIQYLAGLSLPG--NPAIASLMAFTAAVTSPTTSQTL 1182
QY 505 LYE-----AFDEMEECASKAALIEGORMAELKSKIQGLLG----- 541
Db 1183 LFNILGWVAAQLAAPGATAFVAGLAGAALGVSGLGKVLIDILAGYGAGVAGALVAFK 1242
QY 542 -----ILRRHVGGEGAVQWNNRLIAFASGN 568
Db 1243 IMSGEVPTEDLVNLLPAILSPGALVGVWCAAILRRHVGGEGAVQWNNRLIAFASGN 1302
QY 569 HVSPTHVPS----- 578
Db 1303 HVSPTHVPSDAAARVTAISSLTVTOLLRLHQWISSECTTCCSGSLRDIDWICEV 1362
QY 579 ----- 578
Db 1363 LSDFKTLKAKLMPQLPGIPFVSCQGYGVWRVDGIMHTRCHGCAEITGHVKNGTMRIV 1422
QY 579 ----- 578
Db 1423 GPRTCRNWSGTFPINAYTTGCTPLPAPNTYTFALMRVSAEYVEIRQGVDFHYVTGMTT 1482
QY 579 -----RSRREA-----QALPVWARP 594
Db 1483 DNLKPCQVSPSEFTELDGVRLHRFAPCPKLLREEVSFRVGLHEYPVGSQLPCEPEPD 1542
QY 595 Y-----NPP-----LV 600
Db 1543 VAVLTSMLTDFSHITAEAGRLARGSPPSVASSASQSLKATCTANHSDFAELI 1602
QY 601 ET---WKK-----PDYEPVPHG-----RSRRFAQALPV 627
Db 1603 EANLLWRQEMGNITRVESENKVVILDSFDPLVAEEDEREISVPAEILRKSRFAQALPV 1662
QY 628 WARDYNPPLVETWKKPDYEPVPHG 653
Db 1663 WARDYNPPLVETWKKPDYEPVPHG 1688

RESULT 10

AAP92050

ID AAP92050 standard; protein; 2436 AA.

XX

XX

XX

DT 25-MAR-2003 (revised)

DT 02-MAR-1990 (first entry)

XX

XX

DE -1 through 156.

XX

KW Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH).

OS Hepatitis C virus.

XX

FN EP318216-A.

XX

PD 31-MAY-1989.
XX
PF 18-NOV-1988; 88EP-00310922.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
XX
PA (CHIR) CHIRON CORP.
PA (CHIR) CHIRON CORP.
XX
PI Houghton M, Choo QL, Kuo G;
XX
XX WPI; 1989-159274/22.
DR N-ESDB; AAN92106.
XX
XX Purified hepatitis C virus - and associated nucleic acids and polypeptide(s).
PT
PT
XX
PS Claim 13; Fig 47-1-47-8; 139pp; English.
XX
CC It is the sequence encoded in the open reading frame of hepatitis C virus (HCV) cDNA inserts in clones K9-1 through 15e. It is antigenic and could be used in immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A, non-B hepatitis. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
CC
CC
XX
SQ Sequence 2436 AA;
Query Match 36.5%; Score 1624.5; DB 1; Length 2436;
Best Local Similarity 36.1%; Pred. No. 6.9e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 60; Gaps 15;
QY 146 TDNSPPVVPQSFQVLAHPTGSGKSTKVPAAVAAQGYKVLNLPNSVAATLGFAYMSK 205
Db 761 TDNSPPVVPQSFQVLAHPTGSGKSTKVPAAVAAQGYKVLNLPNSVAATLGFAYMSK 820
QY 206 AHGIDPNIRTVRTITGSPITYSTYTKFLADGGCGGAYDIIICDECHSTDAISILGIG 265
Db 821 AHGIDPNIRTVRTITGSPITYSTYTKFLADGGCGGAYDIIICDECHSTDAISILGIG 880
QY 266 TVLQDAETAGARLVVLAATATPPGSVTVPHPNIEEVALSTTGEIPYKAIPLVKGGRH 325
Db 881 TVLQDAETAGARLVVLAATATPPGSVTVPHPNIEEVALSTTGEIPYKAIPLVKGGRH 940
QY 326 LIFCHSKKKCDLAALKVALGINAVAYRGLDVSVIPTSGDVVVVATDALTMTGTDGDFS 385
Db 941 LIFCHSKKKCDLAALKVALGINAVAYRGLDVSVIPTSGDVVVVATDALTMTGTDGDFS 1000
QY 386 VIDNCTC----- 392
Db 1001 VIDNCTCQTQVDFSLDPTFTIETITLPQDAVSTQRRGTRGKPKGIYREVPAGERPSG 1060
QY 393 ----- 392
Db 1061 MFDSSVLCECYDAGCAWVELTPAETTVRLRAYMNTPLGVQCQHLEFWEFVFTGLTHIDA 1120
QY 393 ----- 392
Db 1121 HFLSQTQSGENLPYLVAQATVCARAQPPSWDMQMKLIRLKTPLHGTPLLYRLGA 1180
QY 393 -----ACSG 396
Db 1181 VQNEITLTHPVTKYIMTMSADLEVTSTWLVGVLAALAAAYCLSTGCVVIGRVLSG 1240
QY 397 KPAIIPREVLYRFBDEMECSQHLPYIEQGMMLAEQFKQKALGL-----SRGKPAIVPD 452
Db 1241 KPAIIPREVLYRFBDEMECSQHLPYIEQGMMLAEQFKQKALGLQATASQAE-VIAPA 1299

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QY 453 KEVLYQYD-----EMECSPAAPYIEQAQVIAHQFKEKVLGLDNDQVVVTP-----DKEI 504
DB 1300 VQTNWOKLETFAKHMWNFISGIQVLAGLSTLPG--NPAIASLMAFTAAVTSPLTTSQTL 1357
QY 505 LYE-----AFDEMEECASKAALIEEGORMAEMLSKIQGLLG-----541
DB 1358 LFNILGGWVAAQLAAPGAATAFVGAGLAGAATGSGVLGKVLIDILAGYGAGVAGALVAFK 1417
QY 542 -----ILRRHVGPEGAGVQWNNRLIAFASRGN 568
DB 1418 IMSGEVSPSTEDLVNLLPAILSPGALVGVVCAAILRRHVGPEGAGVQWNNRLIAFASRGN 1477
QY 569 HVSPTHYVPS-----578
DB 1478 HVSPTHYVPSDAAARVTAAILSSLVTQLRLRLHOWISSECTTPCGSWLRDIWDWICEV 1537
QY 579 -----578
DB 1538 LSDEKTLKAKLMPQLPGIPFVSCQRYKGVWRVDGIMHTRCHCGAEITGHVXNGTMRIV 1597
QY 579 -----578
DB 1598 GPRCTCNMWSGTFPINAYTTGCTPLPAPNYTFALMRVSAEYEVVRQVGDPHYVAGMIT 1657
QY 579 -----RSRFA-----QALPVWARD 594
DB 1658 DNLKPCQVSPSEFFTELGDVRLHFPAPCKELLREVSFRVLGHEYPVGSOLPCEPED 1717
QY 595 Y-----NPP-----IV 600
DB 1718 VAVLTSMLTDPSHITAEAGRRLARGSPSVASSASQLSAPSLKATCTANHSDSPAELI 1777
QY 601 ET---WKK-----PDYEPVPHG-----RSSRFAQALPV 627
DB 1778 EANLLWRQMGCGNITRVESENKVVILSDPLVAEEDEREISVPAEILLKSRFAQALPV 1837
QY 628 WARDYNPELVETWKKPDYEPVPHG 653
DB 1838 WARDYNPELVETWKKPDYEPVPHG 1863

RESULT 11
AAP90288
TID AAP90288 standard; protein; 2436 AA.
XX
AC AAP90288;
XX
DT 25-MAR-2003 (revised)
DT 19-JUL-2001 (revised)
DT 01-NOV-1989 (first entry)
XX
DE Peptide encoded by composite hepatitis C cDNA.
XX
KW Hepatitis C virus; clone 15e; clone k9-1; probe; vaccine.
XX
OS Pan troglodytes.
XX
PN GB2212511-A.
XX
PD 26-JUL-1989.
XX
PF 18-NOV-1988; 88GB-00027024.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 26-OCT-1988; 88US-00263584.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Houghton M, Choo QL, Kuo G;
XX
WPI; 1989-215054/30.
DB
```

```
DR N-PSDB; AAN90336.
XX
PT Hepatitis C virus gene - used for prodn. of polynucleotide probes
PT polypeptide(s) and antibodies for diagnosis, prevention and treatment of
PT infection.
XX
PS Disclosure; Fig 47-1 to 47-8; 30pp; English.
XX
CC The sequence is the peptide encoded by the composite hepatitis C virus
CC (HCV) cDNA of AAN90336. The polypeptides are used to diagnose HCV-induced
CC NANBH, to raise antibodies for immunoassay or treatment, or to produce
CC vaccines. (N.B. this record was resubmitted to correct errors in the
CC sequence.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 2436 AA;
Query Match 36.5%; Score 1624.5; DB 1; Length 2436;
Best Local Similarity 36.1%; Pred. No. 6.9e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;
QY 146 TDNSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLPNSVAATLGFAYMSK 205
DB 761 TDNSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLPNSVAATLGFAYMSK 820
QY 206 AHGIDPNRTGVRITTTGSPITYSYGKFLADGGCGGAYDIIICDECHSTDATSILGIG 265
DB 821 AHGIDPNRTGVRITTTGSPITYSYGKFLADGGCGGAYDIIICDECHSTDATSILGIG 880
QY 266 TVLDOAETAGARLVLAATATPGSVTVPHPNIEEVALSTTGEIPYKAIPLVLEIKGRH 325
DB 881 TVLDOAETAGARLVLAATATPGSVTVPHPNIEEVALSTTGEIPYKAIPLVLEIKGRH 940
QY 326 LIFCHSKKCDLAKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDS 385
DB 941 LIFCHSKKCDLAKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDS 1000
QY 386 VIDCNTC-----392
DB 1001 VIDCNTCVTQTVDFSLDFTTETITLPQDAVSRTRQRRGRTGRGKPGIYRFVAPGERPSG 1060
QY 393 -----392
DB 1061 MPDSSVLCEDYDAGCAWVELTPAETTVRLRAYMNTPLPVCQDHLFEHFGVGTGLTHIDA 1120
QY 393 -----392
DB 1121 HFLSQTKSGENLPYLVAQATVCARAQAPPSPBQMWKCLIRLKLPTLHGPTLLYRLGA 1180
QY 393 -----ACSG 396
DB 1181 VQNEITLTHPVTKYIMTCSADLEVVTSTWLVGVLAALAAAYCLSTGCVTVGRVLSG 1240
QY 397 KPAILPDREVLRYRDEMEECSHLPYIEQGMMLAEQFKOKAIGL-----SRGGEPAIVPD 452
DB 1241 KPAILPDREVLRYRDEMEECSHLPYIEQGMMLAEQFKOKAIGLQALGLLTASROAE-VIAPA 1299
QY 453 KEVLYQYD-----EMECSPAAPYIEQAQVIAHQFKEKVLGLDNDQVVVTP-----DKEI 504
DB 1300 VQTNWOKLETFAKHMWNFISGIQVLAGLSTLPG--NPAIASLMAFTAAVTSPLTTSQTL 1357
QY 505 LYE-----AFDEMEECASKAALIEEGORMAEMLSKIQGLLG-----541
DB 1358 LFNILGGWVAAQLAAPGAATAFVGAGLAGAATGSGVLGKVLIDILAGYGAGVAGALVAFK 1417
QY 542 -----ILRRHVGPEGAGVQWNNRLIAFASRGN 568
DB 1418 IMSGEVSPSTEDLVNLLPAILSPGALVGVVCAAILRRHVGPEGAGVQWNNRLIAFASRGN 1477
QY 569 HVSPTHYVPS-----578
DB 1478 HVSPTHYVPSDAAARVTAAILSSLVTQLRLRLHOWISSECTTPCGSWLRDIWDWICEV 1537
QY 579 -----578
DB
```

```
Db 1538 LSDFKTLKAKLMPQLPGIPFVSCQGYKGVWRVYDGMHTRCHGAEITGHVKNKGTMRIV 1597
QY 579 ----- 578
Db 1598 GPRTCRNWSGTFPINAYTTGCTPLPAPNTYFALMRVSAEYVEIRQVGFHYVTQMTT 1657
QY 579 -----RSRREA-----QALPVWARPD 594
Db 1658 DNLKPCQVSPSEFTBLDGVRLHRFAPPCKPLLRBEVSFRVGLHEYPVGSQLPCEPEPD 1717
QY 595 Y-----NPP-----LV 600
Db 1718 VAVLTSMLTDPSSHITAEAGRLARGSPPSVASSASQLSAPSLKATCTANHSDPAELI 1777
QY 601 ET---WKK-----PDYEPVVHG-----RSRRAQALPV 627
Db 1778 EANLLWRQEMGNITRVESENKVVILDSFDPLVAEEDEREISVPAEILRKSRRAQALPV 1837
QY 628 WARDYNPPLVETWKKPDYEPVVHG 653
Db 1838 WAREDYNAPPLVETWKKPDYEPVVHG 1863

RESULT 12
ID AAB18540
XX AAB18540 standard; protein; 2772 AA.
AC AAB18540;
XX
DT 15-JAN-2001 (first entry)
XX
DE Protein encoded by a cDNA compiled Hepatitis C virus cDNA clones.
XX
KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
KW viral infectivity; viral replication.
XX
OS Hepatitis C virus.
XX
PN EP1034785-A2.
XX
PD 13-SEP-2000.
XX
PF 16-MAR-1990; 2000EP-00109602.
XX
PR 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-003411334.
PR 18-MAY-1989; 89US-00355002.
PR 16-MAR-1990; 90EP-00302866.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Houghton M, Choo Q, Kuo G;
XX
DR WPI; 2000-566891/53.
DR N-PSDB; AAA75296.
XX
PT Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.
XX
PS Example; Fig 16; 75pp; English.
XX
CC The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at
CC the polypeptide level to a HCV polyprotein. The antisense polynucleotide
CC binds to cellular polynucleotides which enhance and/or are required for
CC viral infectivity, replicative ability or chronicity. The antisense
CC polynucleotides may also be designed to bind with high specificity, to be
CC of increased stability, to be stable and to have low toxicity. The
CC composition also comprises an agent which causes viral RNA to be
CC inactive. The composition is used for preventing HCV replication in a
```

```
CC system. The present sequence is encoded by a novel HCV cDNA sequence,
CC which is used in the course of the invention
XX
SQ Sequence 2772 AA;
Query Match 36.5%; Score 1624.5; DB 3; Length 2772;
Best Local Similarity 36.1%; Pred. No. 8.2e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;
QY 146 TDNSPPVVFQSFQVAHLHAPTSGSKSTKYPAAAGQYKVLNPNPSVAATLGFAYMSK 205
Db 1097 TDNSPPVVFQSFQVAHLHAPTSGSKSTKYPAAAGQYKVLNPNPSVAATLGFAYMSK 1156
QY 206 AHGIDPNIRTVGRTITTTGSPITTYCKFLADGCGSGAYDIIICDECHSDATSIILGIG 265
Db 1157 AHGIDPNIRTVGRTITTTGSPITTYCKFLADGCGSGAYDIIICDECHSDATSIILGIG 1216
QY 266 TVLDOAETAGARLVVLATATPPGSVTVPHNPNEFVALSTTGEIPFYKAIPLVVIKGRH 325
Db 1217 TVLDOAETAGARLVVLATATPPGSVTVPHNPNEFVALSTTGEIPFYKAIPLVVIKGRH 1276
QY 326 LIFCHSKKCKDELAALVALGINAVAYYRGLDVSVIPTSDDVVVATDALMTGTGDFDS 385
Db 1277 LIFCHSKKCKDELAALVALGINAVAYYRGLDVSVIPTSDDVVVATDALMTGTGDFDS 1336
QY 386 VIDCNTC----- 392
Db 1337 VIDCNTCVTQTVDFSLDPTTETITLTPQDAVSTQRRGRIGRKGPIYRFVAPGERESG 1396
QY 393 ----- 392
Db 1397 MFDSSVLCECYDAGCANVELTPAETTVRLRAYMNTPLGPVQDHLFEWEGVFTGLTHIDA 1456
QY 393 ----- 392
Db 1457 HFLSQTQSGENLPYLVAQYATVCARAQPPSPDWQMKLIRLKLPTLHGTPLLYRGA 1516
QY 393 -----ACSG 396
Db 1517 VQNEITLTHPVTKYIMTMSADLEVTSTWLVGVGLAALAAAYCLSTGCVVIVGRVVLGS 1576
QY 397 KPALIPREVLYREFDEMECSQHLPTYEQMMLEAOFKQKALGI-----SRGKPAIVPD 452
Db 1577 KPALIPREVLYREFDEMECSQHLPTYEQMMLEAOFKQKALGILOQTASQAE--VIAPA 1635
QY 453 KEVLYQQYD-----EMEECSQAAPYIEQAQVIAHQEKVKGLIDNDQVVTP---DKEI 504
Db 1636 VQTNWQKLETFWAKHMNFISGIGYLAGLSTLPG--NPAIASLNAFTAATVSLTTSQTL 1693
QY 505 LYE-----AFDEMEBCASKAALTEEGORMAEMLKSKIQLLG----- 541
Db 1694 LFNILGGWVAQAALAPGAATAFVAGLAGAIGSVGLKVLIDILAGYGAGVAGALVAFK 1753
QY 542 -----ILRRHVGPGEAVQVMNELLIAFASGN 568
Db 1754 IMSGEVFPSTDLVNLPAILSPGALVGVVCAAILRRHVGPGEAVQVMNELLIAFASGN 1813
QY 569 HVSPTHVPS----- 578
Db 1814 HVSPTHVPSDAAARVAILSSLTVQLLRLLHQWISSECTTFCSGSLWRDINDWICEV 1873
QY 579 ----- 578
Db 1874 LSDFKTLKAKLMPQLPGIPFVSCQGYKGVWRVYDGMHTRCHGAEITGHVKNKGTMRIV 1933
QY 579 ----- 578
Db 1934 GPRTCRNWSGTFPINAYTTGCTPLPAPNTYFALMRVSAEYVEIRQVGFHYVTQMTT 1993
QY 579 -----RSRREA-----QALPVWARPD 594
Db 1994 DNLKPCQVSPSEFTBLDGVRLHRFAPPCKPLLRBEVSFRVGLHEYPVGSQLPCEPEPD 2053
```

```
QY 595 Y-----NPP-----IV 600
      :||
Db 2054 VAVLTSMLTDPSHITAEAGRLARGSPPSVASSASQLSAPSLKATCTANHDSDAELI 2113
      :||
QY 601 ET---WK-----PDYEPVVHG-----RSSRFAQALPV 627
      :||
Db 2114 EANLLWRQMGNIIRVSENVKWLDSFDPLVABEDEREISVPAEILKSRFAQALPV 2173
      :||
QY 628 WARDPNPPLVETWKKPDYEPVVHG 653
      :||
Db 2174 WARDPNPPLVETWKKPDYEPVVHG 2199
      :||

RESULT 13
ID AAY14975
AC AAY14975 standard; protein; 2955 AA.
XX AAY14975;
XX
DT 20-MAR-2003 (revised)
DT 08-NOV-1999 (first entry)
XX
XX Amino acid sequence of HCV-1 ORF.
XX
XX Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;
KW HCV infection; vaccine.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 441 /note= "encoded by Tt"
FT Misc-difference 461 /note= "encoded by CCCC"
XX
XX EP939128-A2.
XX
XX 01-SEP-1999.
XX
XX 17-SEP-1990; 99EP-00101746.
XX
XX 15-SEP-1989; 89US-00408045.
XX 21-DEC-1989; 89US-00456142.
XX 17-SEP-1990; 90EP-00310149.
XX
XX (OYAA/) OYA A.
XX (CHIR ) CHIRON CORP.
XX
XX Miyamura T, Saito I, Houghton M, Weiner AJ, Han J, Kolberg JA;
PI Cha T, Irvine BD;
PI
DR WPI; 1999-480843/41.
DR N-PSDB; AAZ07656.
XX
XX New Hepatitis C Virus isolates, useful for diagnosis of hepatitis
PT infections and development of vaccines.
XX
XX Disclosure; Fig 12; 132pp; English.
XX
XX The invention provides two new isolates of hepatitis C virus (HCV), J1
CC and J7. These two isolates comprise nucleotide and amino acid sequences
CC that are distinct from the HCV isolate HCV-1. The nucleotide sequences
CC may be used to detect non-A, non-B HCV (NANBH) polynucleotides by
CC hybridisation for diagnosis of NANBH infections. They may also be used to
CC screen blood donors, donated blood and blood products for this infection.
CC The isolates may also be used to isolate other naturally occurring
CC variants of the virus. The polypeptides may be used as a vaccine for
CC administration to patients to protect against infection with NANBH. The
CC present sequence represents the amino acid sequence of HCV-1 ORF.
CC {Updated on 20-MAR-2003 to correct PF field.} (Updated on 20-MAR-2003 to
CC correct PR field.)
XX
XX Sequence 2955 AA;
```

```
Query Match 36.5%; Score 1624.5; DB 2; Length 2955;
Best Local Similarity 36.1%; Pred. No. 9e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;

QY 146 TDNSPPVPOSFQVAHLHAPTGSKSTKPAAYAAQGYKVLNPSVAATLGFAYMSK 205
      :||
Db 1211 TDNSPPVPOSFQVAHLHAPTGSKSTKPAAYAAQGYKVLNPSVAATLGFAYMSK 1270
      :||
QY 206 AHGIDPNIRTVRTITITGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSI 265
      :||
Db 1271 AHGIDPNIRTVRTITITGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSI 1330
      :||
QY 286 TVLDOAETAGARLVVLTATATPPGSVTVPHPNIEEVALSTTGEIPFYKAIPLV 325
      :||
Db 1331 TVLDOAETAGARLVVLTATATPPGSVTVPHPNIEEVALSTTGEIPFYKAIPLV 1390
      :||
QY 326 LIFCHSKKKCDLAAKLVALGINAVYRGLDVSVIPTSGDVVVVATDALMTGYT 385
      :||
Db 1391 LIFCHSKKKCDLAAKLVALGINAVYRGLDVSVIPTSGDVVVVATDALMTGYT 1450
      :||
QY 386 VIDCNTC----- 392
      :||
Db 1451 VIDCNTCVTQVDFSLDPTFTTITLTPQDAVSRTRGRGTGRGKGIYRFVAP 1510
      :||
QY 393 ----- 392
      :||
Db 1511 MFDSSVLCEYDAGCAWVELTPAETTVRLRAYMNTFGLPVCQDHLFMEGVTF 1570
      :||
QY 393 ----- 392
      :||
Db 1571 HFLSQTOSGENLPYLVAQATVCARAQAPPPSWDMKCLIRLKLPTLHPTPL 1630
      :||
QY 393 -----ACSG 396
      :||
Db 1631 VQNEITLTHPVTKYIMTCSADLEVVSTVVLVGGVLAALAAAYCLSTGCV 1690
      :||
QY 397 KPAIIPDREVLVREPEDEMECSQHLPYIEQGMMLAEQFKQKALGL----- 452
      :||
Db 1691 KPAIIPDREVLVREPEDEMECSQHLPYIEQGMMLAEQFKQKALGLQATASRA 1749
      :||
QY 453 KEVLYQQYD-----EMEECSQAAPYIEQAQVIAHQFKEKVLGLIDNDQV 504
      :||
Db 1750 VQTNWQKLETFWAKHWNPFISQIYLAGLSTUPG--NPAIASLMFTAATVTS 1807
      :||
QY 505 LYE-----AFDEMEECASKALIEEGQRMALMKSITQGLG----- 541
      :||
Db 1808 LFNILGGWVAAQLAAPGAATAFVGAGLAGAAGISVGLGKVLIDILAGYGAG 1867
      :||
QY 542 -----ILRRHVGPGEAGVQWVNRLLIAFASRGN 568
      :||
Db 1868 IMSGEVPESTDLVNLPAILSPGALVGVVCAAILRRHVGPGEAGVQWVNRLL 1927
      :||
QY 569 HVSPHYVPS-----RSRFA-----QALPVWARD 594
      :||
Db 1928 HVSPHYVPSDAAARVTAILLSLVTQLRLRHLHOWISECTTPCSGSLRIND 1987
      :||
QY 579 ----- 578
      :||
Db 1988 LSDFXTLWKLAKLMPQLPGIPFVSCQGYKGVWRVDGMHTRCHCGAEITGH 2047
      :||
QY 579 ----- 578
      :||
Db 2048 GPRCTRNWMSGTFPINAIVTTGCTPLPAPNPTFALWRVSAEYVEIRQVGD 2107
      :||
QY 579 -----RSRFA-----QALPVWARD 594
      :||
Db 2108 DNLCFCQVPSPEPFTDGLVRLHFPAPCKPLLRBEVSRVGLHEYPVGSQPC 2167
      :||
QY 595 Y-----NPP-----IV 600
      :||
Db 2168 VAVLTSMLTDPSHITAEAGRLARGSPPSVASSASQLSAPSLKATCTANHDS 2227
      :||
```

QY 601 ET---WKK-----PDYEPVVHG-----RSSRFAQALPV 627
Db 2228 EANLLWQEMGNITRVESKNVILDSFDPLVAEEDEREISVPAEILRKSRFAQALPV 2287
QY 628 WARDYNPPVETWKKDPYPPVHG 653
Db 2288 WARDYNPPVETWKKDPYPPVHG 2313

RESULT 14

AA18541
ID AAB18541 standard; protein; 2955 AA.

XX AC
XX AAB18541;
XX 15-JAN-2001 (first entry)
XX

XX Polypeptide encoded by sense strand of HCV.

XX Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
XX viral infectivity; viral replication.

XX Hepatitis C virus.

XX EP1034785-A2.

XX 13-SEP-2000.

XX 16-MAR-1990; 2000EP-00109602.

XX 17-MAR-1989; 89US-00325338.

XX 20-APR-1989; 89US-00341334.

XX 18-MAY-1989; 89US-00355002.

XX 16-MAR-1990; 90EP-00302866.

XX (CHIR) CHIRON CORP.

XX Houghton M, Choo Q, Kuo G;

XX WPI; 2000-566891/53.

XX N-PSDB; AAA75297.

XX Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.

XX Example; Fig 17; 75pp; English.

XX The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at
CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide
CC binds to cellular polynucleotides which enhance and/or are required for
CC viral infectivity, replicative ability or chronicity. The antisense
CC polynucleotides may also be designed to bind with high specificity, to be
CC of increased stability, to be stable and to have low toxicity. The
CC composition also comprises an agent which causes viral RNA to be
CC inactive. The composition is used for preventing HCV replication in a
CC system. The present sequence is encoded by a novel HCV cDNA sequence,
CC which is used in the course of the invention

XX Sequence 2955 AA;

XX Query Match 36.5%; Score 1624.5; DB 3; Length 2955;

XX Best Local Similarity 36.1%; Pred. No. 9e-107;

XX Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;

QY 146 TDNSPPVFPQSFQVAHLHAPTGGKSTKVPAAVAAQGYKVLNPNVAATLFGAYMSK 205

Db 1211 TDNSPPVFPQSFQVAHLHAPTGGKSTKVPAAVAAQGYKVLNPNVAATLFGAYMSK 1270

QY 206 AHGIDPNIRTVRTITGSPITYTYGKFLADGCGSGAYDIIICDECHSDATSIILGIG 265

Db 1271 AHGIDPNIRTVRTITGSPITYTYGKFLADGCGSGAYDIIICDECHSDATSIILGIG 1330
QY 266 TVLDOAETAGARLVVLATATPPGSVTVPHNIEVALSTTGEIPYKAIPLVYKGRH 325
Db 1331 TVLDOAETAGARLVVLATATPPGSVTVPHNIEVALSTTGEIPYKAIPLVYKGRH 1390
QY 326 LIFCHSKKCDLAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTGTGDFDS 385
Db 1391 LIFCHSKKCDLAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTGTGDFDS 1450
QY 386 VIDCNC----- 392
Db 1451 VIDCNCVTQTVDFSLDPTFTTITLTPQDAVSITORRGTRGKPGIYRFVAPCRPSG 1510
QY 393 ----- 392
Db 1511 MFDSSVLCEDYACAWVELTPAETTVRLRAYMNTPLPVCQDHLFEPWEGFTGLTHIDA 1570
QY 393 ----- 392
Db 1571 HFLSQTKSGENLPYLVAQATVCARAQAPPSWDQMKCLIRLKLPTLHGFTPLLYLGA 1630
QY 393 -----ACSG 396
Db 1631 VQNEITLTHPVTKYIMTMSADLEVVTSTWLVGGVLAALAAAYCLSTGCVVIVGRVILSG 1690
QY 397 KPAPIPREVLYREFDEMECSQHLPIYEQGMMLAEQFKOKALGL-----SRGKPAIVPD 452
Db 1691 KPAPIPREVLYREFDEMECSQHLPIYEQGMMLAEQFKOKALGLQATASQAB-VIAPA 1749
QY 453 KEVLYQQYD-----EMEECSQAAPYIEQAQVIAHQFKEKVLGLIDNDQVVVTP---DKEI 504
Db 1750 VQTNWQKLETFWAKHWNFISGIQYLAGLSLTPG--NPATASLWAFATAVTSPLTTSQT 1807
QY 505 LYE-----AFDEMECSKAALIEEQORMAEMKSKIQGLLG----- 541
Db 1808 LFNILGGVAAQLAAPGAATAFVAGLAGAAGAGLGLVGLIDILAGYAGVAGALVAFK 1867
QY 542 -----ILRRHVGPGEAGVQMMNRLIAPASRG 568
Db 1868 IMSGEVSTEDLVNMLPAILSPGALVGVVCAALIRRHVGPGEAGVQMMNRLIAPASRG 1927
QY 569 HVSPTHYVPS----- 578
Db 1928 HVSPTHYVPSDAAARVTAIILSLTVTLRLRLHQWISSECTTPCSGSLRDINDWICEV 1987
QY 579 ----- 578
Db 1988 LSDFKTLWAKLMPQLGIPFVSCQGYKGVWRVYDGMHTRCHGCAEITGHVKNGTWRIV 2047
QY 579 ----- 578
Db 2048 GPTRCNWMSGTTPINAYTTGCTPLPAPNYTFALWRVSAEYVEIRQVGFHYVTGMTT 2107
QY 579 -----RSRRFA-----QALPVWARP 594
Db 2108 DNLKCPQVPSBFFTELDGVLRLHFAPCPKPLIREVSRVGLHEYPVGSQLPCEPED 2167
QY 595 Y-----NPP-----LV 600
Db 2168 VAVLTSMLTDPDSHITAEAGRLARGSPFVASSASQLSAPSLKATCTANHDSFDAL 2227
QY 601 ET---WKK-----PDYEPVVHG-----RSSRFAQALPV 627
Db 2228 EANLLWQEMGNITRVESKNVILDSFDPLVAEEDEREISVPAEILRKSRFAQALPV 2287
QY 628 WARDYNPPVETWKKDPYPPVHG 653
Db 2288 WARDYNPPVETWKKDPYPPVHG 2313

RESULT 15
AAR21519

Db 1808 LFNILGGWAAQAAAPGAATAFVAGLAGAAGSGLGKVLIDILAGYGAGVAGALVAFK 1867
QY 542 -----ILRRHVGPGEAVOMNELLIAFASRGN 568
Db 1868 IMSGEVSTEDLVNLLPAILSPGALVGVVCAAILRRHVGPGEAVOMNELLIAFASRGN 1927
QY 569 HVSPTHYVPS-----578
Db 1928 HVSPTHVPSDAAARVAILSSLTVTQLLRHLHQWISSECTTFCSSGSLWLDIWDWICEV 1987
QY 579 -----578
Db 1988 LSDFKTLKAKLMPQLPGIPFVSCQGYKGVVRVDGIMHTRCHCGAEITGHVKNGTMRIV 2047
QY 579 -----578
Db 2048 GPRTCRNMSGTFPPINAYTTGCTPLPAPNTFALWVSAEYVEIROVGFHYVTGWT 2107
QY 579 -----RSTRFA-----QALPVWARPD 594
Db 2108 DNLKPCQVPSPEFTTLDGVRHLRFPAPCKPLLRREYVFRVGLHEYPVGSQLPCEPEPD 2167
QY 595 Y-----NPP-----LV 600
Db 2168 VAVLTSMLTDPSHITAEAGRRRLARGSPSVASSASOLSAPSLKATCTANHDSPDALI 2227
QY 601 ET---WKK-----PDYEPVYHG-----RSTRFAQALPV 627
Db 2228 EANLLRQEMGNGNTRVESENKVVILDSFDPLVAEEDEREISVPAEILKSRFRFAQALPV 2287
QY 628 WARDYNPPLVETWKKPDYEPVYHG 653
Db 2288 WARDYNPPLVETWKKPDYEPVYHG 2313

Search completed: June 21, 2004, 10:30:18
Job time : 64.4736 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2004, 10:18:09 ; Search time 40.9396 Seconds

(without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-2

Perfect score: 3619

Sequence: 1 MAPITAYAQTRGLGLCIIT.....PALIPDREVILXRFDEMEEC 686

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3619	100.0	686	5	Aau76377 Hepatitis
2	3619	100.0	686	5	Aae18689 HCV-1 NS3
3	3619	100.0	686	6	ABG72261 HCV-1 NS3
4	3619	100.0	686	7	ADC06767 HCV mutan
5	3602	99.5	2261	1	AAP90164 Peptide e
6	3602	99.5	2436	1	AAP92050 Sequence
7	3602	99.5	2436	1	AAP90288 Peptide e
8	3602	99.5	2772	3	ABAB18540 Protein e
9	3602	99.5	2955	2	AAV14975 Amino aci
10	3602	99.5	2955	3	ABAB18541 Polyprote
11	3602	99.5	3011	2	AAAR90931 Hepatitis
12	3602	99.5	3011	2	AAW34480 HCV polyp
13	3602	99.5	3011	2	AAW40038 HCV polyp
14	3602	99.5	3011	5	AAE22049 Hepatitis
15	3600	99.5	728	5	AAE18688 NS3/4a mu
16	3600	99.5	728	7	ADC06766 HCV mutan
17	3599	99.4	2301	1	AAAP92047 Sequence
18	3595	99.3	2772	2	AAAR08123 Hepatitis
19	3594	99.3	686	4	ABAB62633 HCV NS3A
20	3593	99.3	3011	2	AAAR21519 Compiled
21	3590	99.2	2435	2	AAAR25135 HCV polyp
22	3589	99.2	3011	2	AAAR31621 Hepatitis
23	3587	99.1	3011	5	AAU84597 HCV polyp
24	3586	99.1	2816	2	AAAR34009 HCV-1 pol
25	3583	99.0	1786	1	AAAP90158 Protein 8

ALIGNMENTS

RESULT 1
AAU76377
ID AAU76377 standard; protein; 686 AA.
XX
AC AAU76377;
XX
DT 08-MAY-2002 (first entry)
XX
DE Hepatitis C virus NS3/4a conformational epitope protein sequence.
XX
KW Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;
KW immunoassay solid support; multiple epitope fusion antigen; MEFA;
KW non-structural protein; mutant; mutein.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 403 /note= "Wild-type Thr substituted by Pro"
FT Misc-difference 404 /note= "Wild-type Ser substituted by Ile"
XX
FN WO200196870-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US019156.
XX
PR 15-JUN-2000; 2000US-0212082P.
PR 02-APR-2001; 2001US-0280811P.
PR 02-APR-2001; 2001US-0280867P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
PI Medina-Selby A;
XX
XX WPI; 2002-090228/12.
DR N-PSDB; ABK15344.
XX
PT Immunoassay solid support, useful for detecting hepatitis C virus
PT infection in biological sample, comprises HCV NS3/4a conformational
PT epitope and multiple epitope fusion antigen bound to the support.
XX
PS Claim 5; Fig 3; 92pp; English.
XX
XX The present invention relates to a new immunoassay solid support
CC

CC consisting essentially of at least one hepatitis C virus (HCV) NS3/4a
CC conformational epitope and a multiple epitope fusion antigen (MEFA),
CC bound to the support. The NS3/4a conformational epitope and/or MEFA
CC reacts specifically with anti-HCV antibodies present in a biological
CC sample from an HCV-infected individual. The immunoassay of the invention
CC is useful for detecting hepatitis C virus infection in a biological
CC sample. The method of the invention provides a sensitive, accurate
CC diagnostic and prognostic tool to provide adequate patient care and to
CC prevent transmission of HCV by blood and by blood products, or by
CC personal contact. Use of NS3/4a conformational epitope in combination
CC with MEFA, provides a sensitive and reliable method for detecting early
CC HCV seroconversion. Use of MEFA has the added advantages of decreasing
CC masking problems, improving sensitivity in detecting antibodies by
CC allowing a greater number of epitopes on a unit surface area of
CC substrate, and improving results. Detection accuracy is increased and
CC the incidence of false results is reduced because of the identification
CC and the use of highly immunogenic HCV antigens which are present during
CC the early stages of HCV seroconversion. The present amino acid sequence
CC represents the non-structural protein NS3/4a conformational epitope of
CC the invention
XX
SQ Sequence 686 AA;
Query Match 100.0%; Score 3619; DB 5; Length 686;
Best Local Similarity 100.0%; Pred. No. 1.6e-306;
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPITAYAAQTRGLGCGIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
DB 1 MAPITAYAAQTRGLGCGIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
QY 61 GTTITASPKGVQIOMYTNVDQDLVGPAPQSGRSLSLTCTCGSSDLYLVTRHADVIPVRRR 120
DB 61 GTTITASPKGVQIOMYTNVDQDLVGPAPQSGRSLSLTCTCGSSDLYLVTRHADVIPVRRR 120
QY 121 GDSRGSLLSPRPISYLVKSGSGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180
DB 121 GDSRGSLLSPRPISYLVKSGSGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180
QY 181 RSPVFTDNSPPVQSFQVAHLHAPTQSGKSTKVPAAQAGYKVLVLPNSVAATLFG 240
DB 181 RSPVFTDNSPPVQSFQVAHLHAPTQSGKSTKVPAAQAGYKVLVLPNSVAATLFG 240
QY 241 AYMSKAGIDNIRGTITGSPITVSTYKFLADGCGSGAYDIIICDECHSTDATS 300
DB 241 AYMSKAGIDNIRGTITGSPITVSTYKFLADGCGSGAYDIIICDECHSTDATS 300
QY 301 ILGIGTVLDQAEATAGARLVILATATPPGSVTVPHENIEEVALSTTGEPFYGKAIPLEVI 360
DB 301 ILGIGTVLDQAEATAGARLVILATATPPGSVTVPHENIEEVALSTTGEPFYGKAIPLEVI 360
QY 361 KGGSHLIFCHSKKKDELAALKVALGINAVAYYRGLDVSVPPIGDDVVVATDMLTGYT 420
DB 361 KGGSHLIFCHSKKKDELAALKVALGINAVAYYRGLDVSVPPIGDDVVVATDMLTGYT 420
QY 421 GDFSDVDCNTCVTQTVDFSLDPTFTIETILPDQAVSRTQRRGTGRKPGIYRFVAPG 480
DB 421 GDFSDVDCNTCVTQTVDFSLDPTFTIETILPDQAVSRTQRRGTGRKPGIYRFVAPG 480
QY 481 ERPSGMPDSSVLCBECYDAGCAWYELTPAETTVLRAYNMTPLGVPQCQDHLFEWGVFTGL 540
DB 481 ERPSGMPDSSVLCBECYDAGCAWYELTPAETTVLRAYNMTPLGVPQCQDHLFEWGVFTGL 540
QY 541 THIDAHFLSQTKSGENIPYLVAQATVCARAQAPPSDQWKKLIRKPTLHGPTPLL 600
DB 541 THIDAHFLSQTKSGENIPYLVAQATVCARAQAPPSDQWKKLIRKPTLHGPTPLL 600
QY 601 YRLGAVQNEIITLTHPVTKYIMTCMSADLEVTSTWLVGGVLAALAAAYCLSTGCWVIYGR 660
DB 601 YRLGAVQNEIITLTHPVTKYIMTCMSADLEVTSTWLVGGVLAALAAAYCLSTGCWVIYGR 660
QY 661 VVLSGKPAIIPDREVLYREFDEMEEC 686
|||||

DB 661 VVLSGKPAIIPDREVLYREFDEMEEC 686

RESULT 2

AAE18689
ID AAE18689 standard; protein; 686 AA.

XX AAE18689;

XX 17-MAY-2002 (first entry)

XX HCV-1 NS3/4a mutant conformational antigen.

XX Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; mutain.

XX Hepatitis C virus type 1.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 403 /note= "Wild type Thr substituted with Pro"

FT Misc-difference 404 /note= "Wild type Ser substituted with Ile"

XX WC200196875-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019369.

XX 15-JUN-2000; 2000US-0212082P.

XX 02-APR-2001; 2001US-0280811P.

XX 02-APR-2001; 2001US-0280867P.

XX (CHIR) CHIRON CORP.

XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

XX Medina-Selby A;

XX WPI; 2002-179522/23.

XX N-PSDB; AAD29795.

XX Immunoassay solid support useful for detecting hepatitis C virus
infection in a biological sample, comprises at least one of HCV anti-core
antibody and HCV NS3/4a epitope, bound to the support.

XX Example 2; Fig 4; 87pp; English.

XX The present invention relates to hepatitis C virus (HCV) core antigen and
NS (nonstructural) 3/4a antibody combination assay that can detect both
HCV antigens and antibodies present in a sample using a single solid
matrix as well as immunoassay solid supports for use in the assay. The
solid support is useful for detecting HCV infection in a biological
sample. The present sequence is HCV-1 NS3/4a mutant conformational
antigen. This sequence is used in the exemplification of the invention

XX Sequence 686 AA;

Query Match 100.0%; Score 3619; DB 5; Length 686;
Best Local Similarity 100.0%; Pred. No. 1.6e-306;
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPITAYAAQTRGLGCGIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 60

DB 1 MAPITAYAAQTRGLGCGIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 60

QY 61 GTTITASPKGVQIOMYTNVDQDLVGPAPQSGRSLSLTCTCGSSDLYLVTRHADVIPVRRR 120

DB 61 GTTITASPKGVQIOMYTNVDQDLVGPAPQSGRSLSLTCTCGSSDLYLVTRHADVIPVRRR 120

QY 121 GDSRGSLLSPRPISYLVKSGSGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180

DB 121 GDSRGSLLSPRPISYLVKSGSGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180

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QY 181 RSPVFTDSSPPVPSQFVAHLHAPTSGSKSTKVPAAVAAQYKVLVLPNSVAATLGF 240
DB 181 RSEVFTDSSPPVPSQFVAHLHAPTSGSKSTKVPAAVAAQYKVLVLPNSVAATLGF 240
QY 241 AYMSKAHGIDPNIRTVRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDATS 300
DB 241 AYMSKAHGIDPNIRTVRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDATS 300
QY 301 ILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVI 360
DB 301 ILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVI 360
QY 361 KGRHLIFCHSKKKDELAALVALGINAVAYRGLDVSVPPIGVVVVATDALMTGYT 420
DB 361 KGRHLIFCHSKKKDELAALVALGINAVAYRGLDVSVPPIGVVVVATDALMTGYT 420
QY 421 GDFSDVIDCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGTGRGKPGIYRFVAPG 480
DB 421 GDFSDVIDCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGTGRGKPGIYRFVAPG 480
QY 481 ERPSGMFDSVLCYDAGCAMELTPAETTVRLRAYMNTPLGVCQDHLEFWEVFTGL 540
DB 481 ERPSGMFDSVLCYDAGCAMELTPAETTVRLRAYMNTPLGVCQDHLEFWEVFTGL 540
QY 541 THIDAHFLSQTQSGENLYIAYQATVCARAQPPSDQWKCLIRLKPILHGTPTLL 600
DB 541 THIDAHFLSQTQSGENLYIAYQATVCARAQPPSDQWKCLIRLKPILHGTPTLL 600
QY 601 YELGAVQNEITLTHPVTKYIMTCMSADLSEVSTWLVGVGLAALAAAYCLSGCVVIVGR 660
DB 601 YELGAVQNEITLTHPVTKYIMTCMSADLSEVSTWLVGVGLAALAAAYCLSGCVVIVGR 660
QY 661 VVLSGKPAIIPDREVLVYREFDEMEEC 686
DB 661 VVLSGKPAIIPDREVLVYREFDEMEEC 686

RESULT 3
ID ABG72261 standard; protein; 686 AA.
AC ABG72261;
DT 06-MAR-2003 (first entry)
DE HCV-1 NS3/4a conformational antigen.
KW Immunoassay solid support; Hepatitis C Virus type-1; HCV-1;
KW NS3/4a conformational epitope; multiple epitope fusion antigen; MEFA;
KW anti-HCV antibody; NS3/4a conformational antigen; HCV infection; mutant;
KW mutcin.
OS Hepatitis C virus type 1.
OS Synthetic.
FH Key
FT Region
FT Location/Qualifiers
FT /note= "Corresponds to amino acid residues 1027-1711 of
FT HCV-1 NS3/4a polypeptide"
FT Misc-difference 403
FT /note= "Substitution of wild-type Thr to Pro"
FT Misc-difference 404
FT /note= "Substitution of wild-type Ser to Ile"
XX US2002146685-A1.
XX 10-OCT-2002.
XX 14-JUN-2001; 2001US-00881654.
XX 15-JUN-2000; 2000US-0212082P.
XX 02-APR-2001; 2001US-0280811P.
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PR 02-APR-2001; 2001US-0280867P.
XX (CHIE/) CHIEN D Y.
PA (ARCA/) ARCANGEL P.
PA (TAND/) TANDESKE L.
PA (GEOR/) GEORGE-NASCIMENTO C.
PA (COIT/) COIT D.
PA (MEDI/) MEDINA-SELBY A.
XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
PI Medina-Selby A;
XX WPI; 2003-147573/14.
DR N-PSDB; ABX14410.
XX Immunoassay solid support for detecting Hepatitis C Virus infection in
PT biological samples, comprises Hepatitis C Virus conformational epitope
PT and multiple epitope fusion antigen.
XX Claim 2; Fig 3A-3D; 45pp; English.
XX The present invention relates to immunoassays comprising Hepatitis C
CC Virus (HCV) NS3/4a conformational epitope and multiple epitope fusion
CC antigen (MEFA), bound to a solid support. The NS3/4a epitope and/or the
CC multiple epitope fusion antigen react with anti-HCV antibodies present in
CC a biological sample from an HCV-infected individual. The immunoassays and
CC methods of the invention are useful for detecting HCV infection in a
CC biological sample. The inventive immunoassay solid support provides a
CC sensitive and reliable method for detecting early HCV seroconversion. The
CC assays can detect HCV infection caused by any six known genotypes of HCV.
CC The use of the multiple epitope fusion proteins decreases masking
CC problems, improves sensitivity in detecting antibodies by allowing a
CC greater number of epitopes on a unit area of substrate, and improves
CC selectivity. The present sequence represents HCV type 1 (HCV-1) NS3/4a
CC conformational antigen, a mutant of the HCV-1 NS3/4a polypeptide
XX Sequence 686 AA;
```

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Query Match 100.0%; Score 3619; DB 6; Length 686;
Best Local Similarity 100.0%; Pred. No. 1.6e-306;
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPITAYAAQTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGCVTWVHGA 60
DB 1 MAPITAYAAQTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGCVTWVHGA 60
QY 61 GTRTIASPKGPVIQMYTNVDQDLVCPAPQSRSLTPTCGSSDLYLVTRHADVIPVRR 120
DB 61 GTRTIASPKGPVIQMYTNVDQDLVCPAPQSRSLTPTCGSSDLYLVTRHADVIPVRR 120
QY 121 GDSRGLSLSPRPISYLVKSGSGGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
DB 121 GDSRGLSLSPRPISYLVKSGSGGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
QY 181 RSPVFTDSSPPVPSQFVAHLHAPTSGSKSTKVPAAVAAQYKVLVLPNSVAATLGF 240
DB 181 RSPVFTDSSPPVPSQFVAHLHAPTSGSKSTKVPAAVAAQYKVLVLPNSVAATLGF 240
QY 241 AYMSKAHGIDPNIRTVRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDATS 300
DB 241 AYMSKAHGIDPNIRTVRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDATS 300
QY 301 ILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVI 360
DB 301 ILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVI 360
QY 361 KGRHLIFCHSKKKDELAALVALGINAVAYRGLDVSVPPIGVVVVATDALMTGYT 420
DB 361 KGRHLIFCHSKKKDELAALVALGINAVAYRGLDVSVPPIGVVVVATDALMTGYT 420
QY 421 GDFSDVIDCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGTGRGKPGIYRFVAPG 480
DB 421 GDFSDVIDCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGTGRGKPGIYRFVAPG 480
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QY 481 ERPSGMDSSVLCYDAGCAWYELTPTAETTVRLRAYMNTPLGVPVCDHLEFWEVFTGL 540
Db 481 ERPSGMDSSVLCYDAGCAWYELTPTAETTVRLRAYMNTPLGVPVCDHLEFWEVFTGL 540
QY 541 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSDQMWKCLIRLKPTELHGPTPLL 600
Db 541 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSDQMWKCLIRLKPTELHGPTPLL 600
QY 601 YRLGAVONEITLTHPVTKYIMTMSADLEVVTSTWLVGGVLAALAYCLSTGCWVIVGR 660
Db 601 YRLGAVONEITLTHPVTKYIMTMSADLEVVTSTWLVGGVLAALAYCLSTGCWVIVGR 660
QY 661 VVLSGKPAIIPDREVLYREFDEMEEC 686
Db 661 VVLSGKPAIIPDREVLYREFDEMEEC 686

RESULT 4
ADC06767
ID ADC06767 standard; protein; 686 AA.
XX AC ADC06767;
XX 18-DEC-2003 (first entry)
DT HCV mutant conformational NS3/4a epitope protein T403P/SA04I.
DE immunosassay solid support; HCV; NS3/4a; non-structural;
XX non-A, non-B hepatitis; NANB; conformational epitope; mutant; muten.
XX Synthetic.
OS Hepatitis C virus.
XX Key Location/Qualifiers
FH Misc-difference 303 /note= "Wild-type Thr replaced by Pro"
FT Misc-difference 304 /note= "Wild-type Ser replaced by Ile"
FT
XX US2002192639-A1.
PN 19-DEC-2002.
XX 14-JUN-2001; 2001US-00881239.
XX 15-JUN-2000; 2000US-0212082P.
PR 02-APR-2001; 2001US-0280811P.
PR 02-APR-2001; 2001US-0280867P.
XX (CHIE/) CHIEN D Y.
PA (ARCA/) ARCANGEL P.
PA (TAND/) TANDESKE L.
PA (GEOR/) GEORGE-NASCIMENTO C.
PA (COIT/) COIT D.
PA (MEDI/) MEDINA-SELBY A.
XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
PI Medina-Selby A;
XX WPI; 2003-644609/61.
DR N-PSDB; ADC06768.
XX Immunosassay solid support for detecting hepatitis C virus infection in
PT biological samples, comprises a hepatitis C virus anti-core antibody and
FT an isolated hepatitis C virus NS3/4a epitope bound HCV anti-core
XX antibody.
XX Claim 6; Fig 4; 40pp; English.
XX The invention relates to a novel immunoassay solid support comprising at
CC least one hepatitis C virus (HCV) anti-core antibody and at least one
XX isolated HCV NS3/4a (non-structural protein 3/4a) epitope bound thereto.

CC The system of the invention may be useful for detecting HCV infection in
CC a biological sample and for treating or detecting non-A, non-B hepatitis
CC (NANB hepatitis). The current sequence is that of the HCV mutant
CC conformational NS3/4a epitope protein of the invention which contains
CC T403P/SA04I mutations.

XX Sequence 686 AA;

Query Match 100.0%; Score 3619; DB 7; Length 686;
Best Local Similarity 100.0%; Pred. No. 1.6e-306;
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPITAYAOQTRGLGCIITSLTRDKNQVEGVQIVSTAAQTFLATCINGCVTVYHGA 60
Db 1 MAPITAYAOQTRGLGCIITSLTRDKNQVEGVQIVSTAAQTFLATCINGCVTVYHGA 60
QY 61 GTRTIASPKGPVIQMTYNVDOLVGPAPQSGSLTCTCGSSDLXLVTRHADVIPVRRR 120
Db 61 GTRTIASPKGPVIQMTYNVDOLVGPAPQSGSLTCTCGSSDLXLVTRHADVIPVRRR 120
QY 121 GDSRGSLLSPRISYILKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180
Db 121 GDSRGSLLSPRISYILKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180
QY 181 RSPVFTDNSSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQYKVLVLPNSVAATLGF 240
Db 181 RSPVFTDNSSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQYKVLVLPNSVAATLGF 240
QY 241 AYSKAHGIDPNRTGVRTITTCSPITYSYGKFLADGGCGGAYDIIICDECHSTDATS 300
Db 241 AYSKAHGIDPNRTGVRTITTCSPITYSYGKFLADGGCGGAYDIIICDECHSTDATS 300
QY 301 ILGIGTVLDOAETAGARLVLAATATPPGVSIVPHNIEEVALSTTGIPFYGKAIPLEVI 360
Db 301 ILGIGTVLDOAETAGARLVLAATATPPGVSIVPHNIEEVALSTTGIPFYGKAIPLEVI 360
QY 361 KGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 420
Db 361 KGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 420
QY 421 GDFSDVIDCNTCVTQTVDFSLDPTTETITLPQAVSRTORRGTRGKGIYRFVAPG 480
Db 421 GDFSDVIDCNTCVTQTVDFSLDPTTETITLPQAVSRTORRGTRGKGIYRFVAPG 480
QY 481 ERPSGMDSSVLCYDAGCAWYELTPTAETTVRLRAYMNTPLGVPVCDHLEFWEVFTGL 540
Db 481 ERPSGMDSSVLCYDAGCAWYELTPTAETTVRLRAYMNTPLGVPVCDHLEFWEVFTGL 540
QY 541 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSDQMWKCLIRLKPTELHGPTPLL 600
Db 541 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSDQMWKCLIRLKPTELHGPTPLL 600
QY 601 YRLGAVONEITLTHPVTKYIMTMSADLEVVTSTWLVGGVLAALAYCLSTGCWVIVGR 660
Db 601 YRLGAVONEITLTHPVTKYIMTMSADLEVVTSTWLVGGVLAALAYCLSTGCWVIVGR 660
QY 661 VVLSGKPAIIPDREVLYREFDEMEEC 686
Db 661 VVLSGKPAIIPDREVLYREFDEMEEC 686

RESULT 5
AAP90164
ID AAP90164 standard; protein; 2261 AA.
XX AC AAP90164;
XX 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)

XX Peptide encoded by composite hepatitis C virus cDNA.
DE Hepatitis C virus; clone 12f; clone 15e; probe; vaccine.
XX

XX Pan troglodytes.
OS
XX GB2212511-A.
PN
XX 26-JUL-1989.
PD
XX 18-NOV-1988; 88GB-00027024.
PF
XX 18-NOV-1987; 87US-00122714.
PR
XX 30-DEC-1987; 87US-00139886.
PR
XX 26-FEB-1988; 88US-00161072.
PR
XX 26-OCT-1988; 88US-00263584.
XX
PA (CHIR) CHIRON CORP.
XX
XX Houghton M, Choo QL, Kuo G;
PI
XX WPI; 1989-215054/30.
DR
XX N-PSDB; AAN90331.
DR
XX
PT Hepatitis C virus gene - used for prodn. of polynucleotide probes
PT polypeptide(s) and antibodies for diagnosis, prevention and treatment of
PT infection.
XX
XX Disclosure; Fig 32; 30pp; English.
XX
XX The sequence is the peptide encoded by the composite hepatitis C virus
CC (HCV) cDNA of AAN90331. The polypeptides are used to diagnose HCV-induced
CC NANBH, to raise antibodies for immunoassay or treatment, or to produce
CC vaccines. (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 2261 AA;
SQ

Query Match 99.5%; Score 3602; DB 1; Length 2261;
Best Local Similarity 99.6%; Pred. No. 2.8e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPITAYAAQQTGRLGCIITSLTGDKKQVEGEVQIVSTAAQTFLATCINGCVWTVYHGA 60
Db :
401 LAPITAYAAQQTGRLGCIITSLTGDKKQVEGEVQIVSTAAQTFLATCINGCVWTVYHGA 460
QY 61 GTRTASPKGPVQIOMVTNVQDLVGMWPAQGSRLTPTCTCGSSDLVLTNRHADVIPVRRR 120
Db 461 GTRTASPKGPVQIOMVTNVQDLVGMWPAQGSRLTPTCTCGSSDLVLTNRHADVIPVRRR 520
QY 121 GDSRGLSPRPISYLKSGSGGPLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
Db 521 GDSRGLSPRPISYLKSGSGGPLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 580
QY 181 RSPVETDNSSPPVQSFQVAHLHAPTKGSKTKVPAAYAAQGYKVLVNPSSVAATLGF 240
Db 581 RSPVETDNSSPPVQSFQVAHLHAPTKGSKTKVPAAYAAQGYKVLVNPSSVAATLGF 640
QY 241 AYMSKAHGIDNIRGVRTITGSPITYSTYKGLADGCGSGAYDIIICDECHSTDATS 300
Db 641 AYMSKAHGIDNIRGVRTITGSPITYSTYKGLADGCGSGAYDIIICDECHSTDATS 700
QY 301 ILGIGTVLDQAEAGARLWLATATPPGSVTVPHNIEVALSTTGEIPFYGKALPLEVI 360
Db 701 ILGIGTVLDQAEAGARLWLATATPPGSVTVPHNIEVALSTTGEIPFYGKALPLEVI 760
QY 361 KGGRLHIECHSKKKCDELAALVALGINAVAYRGLDVSVPPIGDDVVVATDALMTGYT 420
Db 761 KGGRLHIECHSKKKCDELAALVALGINAVAYRGLDVSVPPIGDDVVVATDALMTGYT 820
QY 421 GDFDSVIDNCVTCTVDFSDFTTETITLTPQDAVSRTOBRTGKPGIYRFVAPG 480
Db 821 GDFDSVIDNCVTCTVDFSDFTTETITLTPQDAVSRTOBRTGKPGIYRFVAPG 880
QY 481 ERPSGMFSSVLCYDAGCAWYELTPAETTVRLRAYNNTGFLPVCQDHLFEWEGVFTGL 540
Db 881 ERPSGMFSSVLCYDAGCAWYELTPAETTVRLRAYNNTGFLPVCQDHLFEWEGVFTGL 940

QY 541 THDAHFLSQTKQSGENLPYLVAQATVCARAAQAPPPSWDQMWKCLIRLKPTLHGFTPLL 600
Db 941 THDAHFLSQTKQSGENLPYLVAQATVCARAAQAPPPSWDQMWKCLIRLKPTLHGFTPLL 1000
QY 601 YRLGAVQNEITITLTHPVTKYIMTMSADLEVTSTWLVGCVLAALAAAYCISTGCVVIVGR 660
Db 1001 YRLGAVQNEITITLTHPVTKYIMTMSADLEVTSTWLVGCVLAALAAAYCISTGCVVIVGR 1060
QY 661 VVLSGKPAIIPDREVLRYREFDEMEEC 686
Db 1061 VVLSGKPAIIPDREVLRYREFDEMEEC 1086

RESULT 6
AAP92050
ID AAP92050 standard; protein; 2436 AA.
XX
XX AC AAP92050;
XX
DT 25-MAR-2003 (revised)
DT 02-MAR-1990 (first entry)
XX
DE Sequence encoded in the hepatitis C virus (HCV) cDNA inserts in clones K9
DE -1 through 15e.
XX
XX Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH).
XX Hepatitis C virus.
XX
PN EP318216-A.
XX
PD 31-MAY-1989.
XX
XX 18-NOV-1988; 88EP-00310922.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
XX
PA (CHIR) CHIRON CORP.
PA (CHIR) CHIRON CORP.
XX
PI Houghton M, Choo QL, Kuo G;
XX
DR WPI; 1989-159274/22.
DR N-PSDB; AAN92106.
XX
PT Purified hepatitis C virus - and associated nucleic acids and
PT polypeptide(s).
XX
PS Claim 13; Fig 47-1-47-8; 139pp; English.
XX
CC It is the sequence encoded in the open reading frame of hepatitis C virus
CC (HCV) cDNA inserts in clones K9-1 through 15e. It is antigenic and could
CC be used in immunoassay reagents and vaccines and to generate antibodies
CC useful in diagnosis and passive immunotherapy for HCV infection/non-A,
CC non-B hepatitis. (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 2436 AA;

Query Match 99.5%; Score 3602; DB 1; Length 2436;
Best Local Similarity 99.6%; Pred. No. 3.1e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPITAYAAQQTGRLGCIITSLTGDKKQVEGEVQIVSTAAQTFLATCINGCVWTVYHGA 60
Db 576 LAPITAYAAQQTGRLGCIITSLTGDKKQVEGEVQIVSTAAQTFLATCINGCVWTVYHGA 635

RESULT 8
AA18540
ID AAB18540 standard; protein; 2772 AA.
XX AC AAB18540;
XX DT 15-JAN-2001 (first entry)
XX DE Protein encoded by a cDNA compiled Hepatitis C virus cDNA clones.
XX KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
XX KW viral infectivity; viral replication.
XX OS Hepatitis C virus.
XX PN EP1034785-A2.
XX PD 13-SEP-2000.
XX PF 16-MAR-1990; 2000EP-00109602.
XX PR 17-MAR-1989; 89US-00325338.
XX PR 20-APR-1989; 89US-00341334.
XX PR 18-MAY-1989; 89US-00355002.
XX PR 16-MAR-1990; 90EP-00302866.
XX (CHIR) CHIRON CORP.
XX Houghton M, Choo Q, Kuo G;
XX WPI; 2000-566891/53.
XX N-PSDB; AAA75296.

Novel composition comprising a hepatitis C virus antisense polynucleotide which is complementary to or corresponds to a sense strand of the virus genome, and selectively hybridizes to it.
Example; Fig 16; 75pp; English.

The specification describes a pharmaceutical composition which comprises a hepatitis C virus (HCV) antisense polynucleotide. The HCV is characterized by a positive stranded RNA genome which has 40% homology at the polypeptide level to a HCV polypeptide. The antisense polynucleotide binds to cellular polynucleotides which enhance and/or are required for viral infectivity, replicative ability or chronicity. The antisense polynucleotides may also be designed to bind with high specificity, to be of increased stability, to be stable and to have low toxicity. The composition also comprises an agent which causes viral RNA to be inactive. The composition is used for preventing HCV replication in a system. The present sequence is encoded by a novel HCV cDNA sequence, which is used in the course of the invention

Query Match 99.5%; Score 3602; DB 3; Length 2772;
Best Local Similarity 99.6%; Pred. No. 3.8e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MAPITAYAAQQTGRLGCIITSITGRDKNOVEGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
912 LAPITAYAAQQTGRLGCIITSITGRDKNOVEGEVQIVSTAAQTFLATCINGVCWTVYHGA 971
61 GTRTIASPKGPVQMYTNVDQDLVGPAPQGRSLTPTCTGSSDLYLVTRHADVIPVRR 120
972 GTRTIASPKGPVQMYTNVDQDLVGPAPQGRSLTPTCTGSSDLYLVTRHADVIPVRR 1031
121 GDSRGLSPRPISVLKSSGGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
1032 GDSRGLSPRPISVLKSSGGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 1091
181 RSPVFTDNSSPPVPPQSFQVAHLHAPTSGKSTKVPAAAYAGQYKVLNPSVAATLFG 240
1092 RSPVFTDNSSPPVPPQSFQVAHLHAPTSGKSTKVPAAAYAGQYKVLNPSVAATLFG 1151

QY 241 AYMSKAHGIDENIRTVRTITITGSPITYTYGKFLADGCGSGGAYDIIICDECHSTDATS 300
Db 1152 AYMSKAHGIDENIRTVRTITITGSPITYTYGKFLADGCGSGGAYDIIICDECHSTDATS 1211
QY 301 ILGIGTVLDQAEATAGARLVVLTATPPGCVTVPHENIEEVALSTTGEIFFYKKAIPLEVI 360
Db 1212 ILGIGTVLDQAEATAGARLVVLTATPPGCVTVPHENIEEVALSTTGEIFFYKKAIPLEVI 1271
QY 361 KGGRHILFCHSKKKCDELAALVALGINAVAYYRGLDVSVIPPIGDVVVWATDALMTGVT 420
Db 1272 KGGRHILFCHSKKKCDELAALVALGINAVAYYRGLDVSVIPTSGDVVVWATDALMTGVT 1331
QY 421 GDFSDVIDCNTCVTQTVDFSLDPTFTTETITLPQDAVSRTQRRGTGRKPGIYRFVAPG 480
Db 1332 GDFSDVIDCNTCVTQTVDFSLDPTFTTETITLPQDAVSRTQRRGTGRKPGIYRFVAPG 1391
QY 481 ERPSGMFDSVLCRCYDAGCAWYELTPAETTVRLRAYNTPGLPVCQDHLFEWGVFTGL 540
Db 1392 ERPSGMFDSVLCRCYDAGCAWYELTPAETTVRLRAYNTPGLPVCQDHLFEWGVFTGL 1451
QY 541 THIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQWKKLIRLKPILHGPTELL 600
Db 1452 THIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQWKKLIRLKPILHGPTELL 1511
QY 601 YRLGAVQNEITLTHPVTKYIMTMSADLEVVITSTWLVGGVLAALAAAYCLSTGCVVIVGR 660
Db 1512 YRLGAVQNEITLTHPVTKYIMTMSADLEVVITSTWLVGGVLAALAAAYCLSTGCVVIVGR 1571
QY 661 VVLSGKPAIIPDREVLVREDFEMEEC 686
Db 1572 VVLSGKPAIIPDREVLVREDFEMEEC 1597

RESULT 9

AA14975
ID AAY14975 standard; protein; 2955 AA.
XX AC AAY14975;
XX DT 20-MAR-2003 (revised)
XX DT 08-NOV-1999 (first entry)
XX DE Amino acid sequence of HCV-1 ORF.
XX KW Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;
XX KW HCV infection; vaccine.
XX OS Hepatitis C virus.
XX FH Key Location/Qualifiers
FT Misc-difference 441 /note= "encoded by TT"
FT FT Misc-difference 461 /note= "encoded by CCCC"
XX PN EP939128-A2.
XX PD 01-SEP-1999.
XX PF 17-SEP-1990; 99EP-00101746.
XX PR 15-SEP-1989; 89US-00408045.
XX PR 21-DEC-1989; 89US-00456142.
XX PR 17-SEP-1990; 90EP-00310149.
XX (OYAA/) OYA A.
XX (CHIR) CHIRON CORP.

PI Miyamura T, Saito I, Houghton M, Weiner AJ, Han J, Kolberg JA;
XX Cha T, Irvine BD;
XX WPI; 1999-480843/41.

DR N-PSDB; AAZ07656.
XX New Hepatitis C Virus isolates, useful for diagnosis of hepatitis
PT infections and development of vaccines.
XX
XX Disclosure; Fig 12; 132pp; English.
XX
XX The invention provides two new isolates of hepatitis C virus (HCV), J1
CC and J7. These two isolates comprise nucleotide and amino acid sequences
CC that are distinct from the HCV isolate HCV-1. The nucleotide sequences
CC may be used to detect non-A, non-B HCV (NANBH) polynucleotides by
CC hybridisation for diagnosis of NANBH infections. They may also be used to
CC screen blood donors, donated blood and blood products for this infection.
CC The isolates may also be used to isolate other naturally occurring
CC variants of the virus. The polypeptides may be used as a vaccine for
CC administration to patients to protect against infection with NANBH. The
CC present sequence represents the amino acid sequence of HCV-1 ORF.
CC (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 2955 AA;

Query Match 99.5%; Score 3602; DB 2; Length 2955;
Best Local Similarity 99.6%; Pred. No. 4.2e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPITAAQOTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVVHGA 60
Db :|||||
QY 1026 LAPITAAQOTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVVHGA 1085
Db :|||||
QY 61 GTTITASPKGPVIMYTNVDQDLVGPAPQGSRLTPTCTCGSSDLYLVTTHADVIPVRRR 120
Db :|||||
QY 1086 GTRITASPKGPVIMYTNVDQDLVGPAPQGSRLTPTCTCGSSDLYLVTTHADVIPVRRR 1145
Db :|||||
QY 121 GDSRGSLLSPRIYLYKSGSGGGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
Db :|||||
QY 1146 GDSRGSLLSPRIYLYKSGSGGGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 1205
Db :|||||
QY 181 RSPVFTDSSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPSPVAATLGF 240
Db :|||||
QY 1206 RSPVFTDSSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPSPVAATLGF 1265
Db :|||||
QY 241 AYMSKAHGIDPNIRTVGRTITTSPIYTYGKFLADGCGSGGAYDIIICDECHSTDATS 300
Db :|||||
QY 1266 AYMSKAHGIDPNIRTVGRTITTSPIYTYGKFLADGCGSGGAYDIIICDECHSTDATS 1325
Db :|||||
QY 301 ILGIGTVLDOAETAGARLVLAATPPGCVTVVHPNIEEVALSTTGIPYKGAIPLEVI 360
Db :|||||
QY 1326 ILGIGTVLDOAETAGARLVLAATPPGCVTVVHPNIEEVALSTTGIPYKGAIPLEVI 1385
Db :|||||
QY 361 KGRHLLIFCHSKKCDLAKLVALGINAVAYRGLDVSVIPPIGDVVVATDALTMTGYT 420
Db :|||||
QY 1386 KGRHLLIFCHSKKCDLAKLVALGINAVAYRGLDVSVIPPIGDVVVATDALTMTGYT 1445
Db :|||||
QY 421 GDFDSVIDCNTCVTQTVDLDFPTTETITLPQDAVSRTOQRGRGKPGIYRFVAPG 480
Db :|||||
QY 1446 GDFDSVIDCNTCVTQTVDLDFPTTETITLPQDAVSRTOQRGRGKPGIYRFVAPG 1505
Db :|||||
QY 481 ERPSGMPDSSVLCBCYDAGCAWYELTAEFTTVRLRAYMTPEGLPYCODHLEFWEQVETGL 540
Db :|||||
QY 1506 ERPSGMPDSSVLCBCYDAGCAWYELTAEFTTVRLRAYMTPEGLPYCODHLEFWEQVETGL 1565
Db :|||||
QY 541 THIDAHFSLQTSQSGENLPYLVAQVTCARAAQPPPSQWQMKLLIRLKPTLHGPTPLL 600
Db :|||||
QY 1566 THIDAHFSLQTSQSGENLPYLVAQVTCARAAQPPPSQWQMKLLIRLKPTLHGPTPLL 1625
Db :|||||
QY 601 YRLGAVONEITLTHPVTKYIMTCMSADLEVTSTWLVGVGLAALAYCLSTGCWTVVGR 660
Db :|||||
QY 1626 YRLGAVONEITLTHPVTKYIMTCMSADLEVTSTWLVGVGLAALAYCLSTGCWTVVGR 1685
Db :|||||
QY 661 VVLGSKPAITPDREVLYRFEDEMEEC 686
Db :|||||
QY 1686 VVLGSKPAITPDREVLYRFEDEMEEC 1711
Db :|||||

RESULT 10
AAB18541
ID AAB18541 standard; protein; 2955 AA.
XX
XX AAB18541;
AC
XX
XX 15-JAN-2001 (first entry)
DT
XX
XX Polypeptide encoded by sense strand of HCV.
DE
XX
XX Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
KW viral infectivity; viral replication.
KW
XX
XX Hepatitis C virus.
OS
XX
XX EP1034785-A2.
PN
XX
XX 13-SEP-2000.
PD
XX
XX 16-MAR-1990; 2000EP-00109602.
PF
XX
XX 17-MAR-1989; 89US-00325338.
PR
XX
XX 20-APR-1989; 89US-00341334.
PR
XX
XX 18-MAY-1989; 89US-00355002.
PR
XX
XX 16-MAR-1990; 90EP-00302866.
PR
XX
XX (CHIR) CHIRON CORP.
PA
XX
XX Houghton M, Choo Q, Kuo G;
PI
XX
XX WPI; 2000-566891/53.
DR
XX
XX N-PSDB; AAA75297.
XX
XX Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.
PT
XX
XX Example; Fig 17; 75pp; English.
PS
XX
XX The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at
CC the polypeptide level to a HCV polyprotein. The antisense polynucleotide
CC binds to cellular polynucleotides which enhance and/or are required for
CC viral infectivity, replicative ability or chronicity. The antisense
CC polynucleotides may also be designed to bind with high specificity, to be
CC of increased stability, to be stable and to have low toxicity. The
CC composition also comprises an agent which causes viral RNA to be
CC inactive. The composition is used for preventing HCV replication in a
CC system. The present sequence is encoded by a novel HCV cDNA sequence,
CC which is used in the course of the invention
XX
SQ Sequence 2955 AA;

Query Match 99.5%; Score 3602; DB 3; Length 2955;
Best Local Similarity 99.6%; Pred. No. 4.2e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPITAAQOTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVVHGA 60
Db :|||||
QY 1026 LAPITAAQOTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVVHGA 1085
Db :|||||
QY 61 GTTITASPKGPVIMYTNVDQDLVGPAPQGSRLTPTCTCGSSDLYLVTTHADVIPVRRR 120
Db :|||||
QY 1086 GTRITASPKGPVIMYTNVDQDLVGPAPQGSRLTPTCTCGSSDLYLVTTHADVIPVRRR 1145
Db :|||||
QY 121 GDSRGSLLSPRIYLYKSGSGGGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
Db :|||||
QY 1146 GDSRGSLLSPRIYLYKSGSGGGLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 1205
Db :|||||
QY 181 RSPVFTDSSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPSPVAATLGF 240
Db :|||||


```
Db 1206 RSPVFTDNSSPPVPSQSFQVAHLHAPTSGKSTKVPAAAYAGKYKVLNPSVAATLFGF 1265
QY 241 AYMSKAHGIDPNIRTCVRIITGSPITYSTYKFLADGGCGGAYDIIICDCHSTDATS 300
Db 1266 AYMSKAHGIDPNIRTCVRIITGSPITYSTYKFLADGGCGGAYDIIICDCHSTDATS 1325
QY 301 ILGIGTVLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYKALPLEVI 360
Db 1326 ILGIGTVLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYKALPLEVI 1385
QY 361 KGRHLIFCHSKKKCDELAALKI VALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 420
Db 1386 KGRHLIFCHSKKKCDELAALKI VALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 1445
QY 421 GDFDSVIDCNTCVTQTVDPSLDPTFTIETITL PQDAVSRTOGRGTGRGKPGIYRFVAPG 480
Db 1446 GDFDSVIDCNTCVTQTVDPSLDPTFTIETITL PQDAVSRTOGRGTGRGKPGIYRFVAPG 1505
QY 481 ERPSGMFSSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPLGVCQDHLFEWEGVFTGL 540
Db 1506 ERPSGMFSSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPLGVCQDHLFEWEGVFTGL 1565
QY 541 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQWKCLIRLKP TLHGPTPL 600
Db 1566 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQWKCLIRLKP TLHGPTPL 1625
QY 601 YRLGAVQNEITLTHPVTKYIMTCSADLEVVSTWVLVGGVLAALAAAYCLSTGCVVIVGR 660
Db 1626 YRLGAVQNEITLTHPVTKYIMTCSADLEVVSTWVLVGGVLAALAAAYCLSTGCVVIVGR 1685
QY 661 VVLSGKPAIIPDREVLYREFDEMEEC 686
Db 1686 VVLSGKPAIIPDREVLYREFDEMEEC 1711

RESULT 11
AAR90931
ID AAR90931 standard; protein; 3011 AA.
XX AC AAR90931;
XX AC AAR90931;
DT 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
DE Hepatitis C virus polyprotein.
KW Non-A non-B hepatitis virus; NANBHV; HCV; antigen; detection; diagnosis;
KW antibodies.
XX Hepatitis C virus.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT Misc-difference 1..122 /label= antigen
FT /label= "C22; AAR90936"
FT /note= "C22; AAR90936"
FT Misc-difference 199..328
FT /label= antigen
FT /note= "S2; AAR90935"
FT Misc-difference 1192..1457
FT /label= antigen
FT /note= "C33c; AAR90932"
FT Misc-difference 1569..1931
FT /label= antigen
FT /note= "C100; AAR90933"
FT Misc-difference 2054..2464
FT /label= antigen
FT /note= "NS5; AAR90934"
XX
PN EP693687-A1.
XX
PD 24-JAN-1996.
XX
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PF 03-APR-1991; 95EP-00114016.
XX
PR 04-APR-1990; 90US-00504352.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Houghton M, Choo Q, Kuo G;
XX
DR WPI; 1996-117956/13.
DR N-PSDB; AAT12710.
XX
PT Combinations of synthetic Hepatitis C Virus antigens - provide more
PT effective diagnosis of Non-A, Non-B Hepatitis.
XX
PS Disclosure; Fig 1(A-Y); 53pp; English.
XX
CC The combination comprises an HCV antigen from the C domain (pref. C22 -
CC AAR90936) and at least one HCV antigen from the NS3 (pref. C33c - or NS5
CC AAR90932), NS4 (pref. C100 - AAR90933), S (pref. S2 - AAR90935) or NS5
CC (AAR90934) domain. The antigens may in the form of a fusion protein, a
CC simple physical mixture, or the individual antigens commonly bound to a
CC solid matrix. They are pref. prepd. by recombinant DNA techniques
CC (primers are given in AAT12711-T12716), but can be synthesised or
CC isolated from HCV using affinity chromatography. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 3011 AA;
Query Match 99.5%; Score 3602; DB 2; Length 3011;
Best Local Similarity 99.6%; Pred. No. 4.3e-304; Mismatches 1; Indels 0; Gaps 0;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MAPITAYAAQOTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
Db 1026 LAPITAYAAQOTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA 1085
QY 61 GTRTIASPKGPVIQMYTNVDQDLVGNWPAPOGSRSLTPTCTCGSSDLYLTVRHDVTPVRRR 120
Db 1086 GTRTIASPKGPVIQMYTNVDQDLVGNWPAPOGSRSLTPTCTCGSSDLYLTVRHDVTPVRRR 1145
QY 121 GDSRGLSPRIPI SYLKGSSGGLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETMM 180
Db 1146 GDSRGLSPRIPI SYLKGSSGGLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETMM 1205
QY 181 RSPVFTDNSSPPVPSQSFQVAHLHAPTSGKSTKVPAAAYAGKYKVLNPSVAATLFGF 240
Db 1206 RSPVFTDNSSPPVPSQSFQVAHLHAPTSGKSTKVPAAAYAGKYKVLNPSVAATLFGF 1265
QY 241 AYMSKAHGIDPNIRTCVRIITGSPITYSTYKFLADGGCGGAYDIIICDCHSTDATS 300
Db 1266 AYMSKAHGIDPNIRTCVRIITGSPITYSTYKFLADGGCGGAYDIIICDCHSTDATS 1325
QY 301 ILGIGTVLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYKALPLEVI 360
Db 1326 ILGIGTVLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYKALPLEVI 1385
QY 361 KGRHLIFCHSKKKCDELAALKI VALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 420
Db 1386 KGRHLIFCHSKKKCDELAALKI VALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 1445
QY 421 GDFDSVIDCNTCVTQTVDPSLDPTFTIETITL PQDAVSRTOGRGTGRGKPGIYRFVAPG 480
Db 1446 GDFDSVIDCNTCVTQTVDPSLDPTFTIETITL PQDAVSRTOGRGTGRGKPGIYRFVAPG 1505
QY 481 ERPSGMFSSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPLGVCQDHLFEWEGVFTGL 540
Db 1506 ERPSGMFSSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPLGVCQDHLFEWEGVFTGL 1565
QY 541 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQWKCLIRLKP TLHGPTPL 600
Db 1566 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQWKCLIRLKP TLHGPTPL 1625
QY 601 YRLGAVQNEITLTHPVTKYIMTCSADLEVVSTWVLVGGVLAALAAAYCLSTGCVVIVGR 660
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Db 1626 YRLGAVQNEILTHPTVKYINTOMSADELVSTWVLGGVLAALAAAYCLSTGCVIIGR 1685
Qy 661 VVLSGKPAIIPDREVLVREDEMEEC 686
Db 1686 VVLSGKPAIIPDREVLVREDEMEEC 1711

RESULT 12
AAW34480
ID AAW34480 standard; protein; 3011 AA.
XX AC AAW34480;
XX DT 25-MAR-2003 (revised)
DT 16-MAR-1998 (first entry)
XX DE HCV polyprotein.
XX KW PCR primer; amplify; HCV; hepatitis c virus; antigen combination; NS3;
KW C domain; S domain; NS5; HCV polyprotein; anti-HCV antibody; detection;
XX NS4.
XX OS Hepatitis C virus.
XX PH Location/Qualifiers
FT Misc-difference 366 /note= "can optionally be Arg"
FT Misc-difference 372 /note= "can optionally be Thr"
FT Misc-difference 867 /note= "can optionally be Thr"
FT Misc-difference 1341 /note= "can optionally be Thr"
FT Misc-difference 1341 /note= "can optionally be Val"
FT Misc-difference 2148 /note= "can optionally be Ile"
FT Misc-difference 2883 /note= "can optionally be Asn"
FT Misc-difference 3681 /note= "can optionally be Ser"
FT Misc-difference 3690 /note= "can optionally be Thr"
FT Misc-difference 4167 /note= "can optionally be Leu"
FT Misc-difference 4323 /note= "can optionally be Val"
FT Misc-difference 4701 /note= "can optionally be Tyr"
FT Misc-difference 4752 /note= "can optionally be Ser"
FT Misc-difference 5970 /note= "can optionally be Gly"
FT Misc-difference 6183 /note= "can optionally be His"
FT Misc-difference 6186 /note= "can optionally be Cys"
FT Misc-difference 6402 /note= "can optionally be Val"
FT Misc-difference 7386 /note= "can optionally be Ser"
FT Misc-difference 7494 /note= "can optionally be Phe"
FT Misc-difference 7497 /note= "can optionally be Ala"
FT Misc-difference 7845 /note= "can optionally be Phe"
FT Misc-difference 8409 /note= "can optionally be Gly"
FT Misc-difference 9102 /note= "can optionally be Gly"
FT Misc-difference 9327 /note= "can optionally be Pro"
XX
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```
PN US5683864-A.
XX 04-NOV-1997.
XX 07-JUL-1992; 92US-00910760.
XX 18-NOV-1987; 87US-00122714.
XX 30-DEC-1987; 87US-00139886.
XX 26-FEB-1988; 88US-00161072.
XX 06-MAY-1988; 88US-00191263.
XX 26-OCT-1988; 88US-00263584.
XX 14-NOV-1988; 88US-00271450.
XX 17-MAR-1989; 89US-00325338.
XX 20-APR-1989; 89US-00341334.
XX 21-APR-1989; 89US-00353896.
XX 18-MAY-1989; 89US-00355002.
XX 04-APR-1990; 90US-00504352.
XX (CHIR ) CHIRON CORP.
XX Kuo G, Houghton M, Choo Q;
XX WPI; 1997-5489976/50.
XX N-PSDB; AAT99981.
XX Combination of three hepatitis C virus antigens - used for detection of
XX specific antibodies to diagnose infection.
XX Disclosure; Col 25-46; 57pp; English.
XX This sequence represents the Hepatitis C virus polyprotein. Fragments of
XX the DNA encoding this sequence can be amplified and used in the
XX combination of HCV antigens of the invention. The HCV antigen combination
XX comprises an antigen (Ag1) comprising the C domain (i.e. amino acids (aa)
XX 1-120 of the HCV polyprotein), or its immunologically reactive fragment
XX containing at least 8 aa. It also comprises two additional antigens from
XX two different polyprotein domains, including at least 8 aa from the NS3,
XX NS4, S or NS5 domains of the polyprotein, corresponding, respectively, to
XX aa 1050-1640; 1640-2000; 120-400 and 2000-3011 of the HCV polyprotein.
XX Alternatively, Ag1 contains at least 8 aa from the 1-122 or 9-177 aa
XX regions of the HCV polyprotein. These antigen combinations are used
XX diagnostically to detect anti-HCV antibodies, using any standard
XX immunoassay format. These antigen combinations have a broader range of
XX reactivity with antibodies than any antigen individually. (Updated on 25-
XX MAR-2003 to correct PR field.)
XX SQ Sequence 3011 AA;
Query Match 99.5%; Score 3602; DH 2; Length 3011;
Best Local Similarity 99.6%; Pred. No. 4.3e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MAPITAYAQTRGLLGCIIITSLTGRDNQVEGEVQIVSTAAQTFLATCINGVCVTVHGA 60
Db 1026 LAPITAYAQTRGLLGCIIITSLTGRDNQVEGEVQIVSTAAQTFLATCINGVCVTVHGA 1085
Qy 61 GTRTIASPKGFVIOMYTNVDQDLVGWPAQSGSLTPTCTGSSDLXLVTRHADVIPVRRR 120
Db 1086 GTRTIASPKGFVIOMYTNVDQDLVGWPAQSGSLTPTCTGSSDLXLVTRHADVIPVRRR 1145
Qy 121 GDSRGSLLSPRISYLVKSGSGGPLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
Db 1146 GDSRGSLLSPRISYLVKSGSGGPLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 1205
Qy 181 RSPVFTDNSSPPVYVQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLPNSVAATLGF 240
Db 1206 RSPVFTDNSSPPVYVQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLPNSVAATLGF 1265
Qy 241 AYMSKAHGIDENIRTVRTITTTGSPITYSTYTGKFLADGGCGGGAYDIIICDCHSTDATS 300
Db 1266 AYMSKAHGIDENIRTVRTITTTGSPITYSTYTGKFLADGGCGGGAYDIIICDCHSTDATS 1325
Qy 301 ILGIGTVLDQAFETAGARLVVLATATPFGSVTVPHNIEEVALSTGTGEIPFGKALPLEVI 360
```

```
Db      1326  ILGIGTVLQDAETAGARLVLAATPPGVTVPHPNIEEVALSTTGEIPFYGKAIPLEVI 1385
QY      361  KGRHLIFCHSKKKDELAAKLVAGINAVAYRGLDVSVIPPIGDDVVVVATDALTMTGYT 420
Db      1386  KGRHLIFCHSKKKDELAAKLVAGINAVAYRGLDVSVIPISGDDVVVVATDALTMTGYT 1445
QY      421  GPDFSVIDNCNTCVTQVDFSLDPTFTIETITLPQDAVSRTRGRGKPGIYRFVAPG 480
Db      1446  GPDFSVIDNCNTCVTQVDFSLDPTFTIETITLPQDAVSRTRGRGKPGIYRFVAPG 1505
QY      481  EPPSGMFDSSVLCECYDAGCAWVELTPARTTVLRAYMNTPGIPVQDHLFEWEGVFTGL 540
Db      1506  EPPSGMFDSSVLCECYDAGCAWVELTPARTTVLRAYMNTPGIPVQDHLFEWEGVFTGL 1565
QY      541  THIDAHFLSQTKSGENLPYLVAQATVCARQAAPPSPWDQWKKLIRLKPILHGTPPLL 600
Db      1566  THIDAHFLSQTKSGENLPYLVAQATVCARQAAPPSPWDQWKKLIRLKPILHGTPPLL 1625
QY      601  YRLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWLVGGVLAALAAAYCLSTGCVVIVGR 660
Db      1626  YRLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWLVGGVLAALAAAYCLSTGCVVIVGR 1685
QY      661  VVLSGKPAIIPREVLYRPFDEMEEC 686
Db      1686  VVLSGKPAIIPREVLYRPFDEMEEC 1711

RESULT 13
AAW40038
ID  AAW40038 standard; protein; 3011 AA.
AC  AAW40038;
XX
XX
DT  26-MAY-1998 (first entry)
DE  HCV polyprotein.
XX
KW  Hepatitis C virus C domain; HCV; C antigen; immunological activity;
XX  NS3 domain; NS4 domain; S domain; NS5 domain.
OS  Hepatitis C virus.
XX
FH  Key Location/Qualifiers
FT  Domain 1..120
FT  /label= C_domain
FT  Modified-site 9
FT  /note= "As given in the specification this amino acid can
FT  also be Arg"
FT  Modified-site 11
FT  /note= "As given in the specification this amino acid can
FT  also be Thr"
FT  Domain 120..400
FT  /label= S_domain
FT  Modified-site 174
FT  /note= "As given in the specification this amino acid can
FT  also be Thr"
FT  Modified-site 334
FT  /note= "As given in the specification this amino acid can
FT  also be Val"
FT  Modified-site 603
FT  /note= "As given in the specification this amino acid can
FT  also be Ile"
FT  Modified-site 847
FT  /note= "As given in the specification this amino acid can
FT  also be Asn"
FT  Domain 1050..1640
FT  /label= NS3_domain
FT  Modified-site 1114
FT  /note= "As given in the specification this amino acid can
FT  also be Ser"
FT  Modified-site 1217
FT  /note= "As given in the specification this amino acid can
```

```
FT  also be Thr"
FT  Modified-site 1276
FT  /note= "As given in the specification this amino acid can
FT  also be Leu"
FT  Modified-site 1328
FT  /note= "As given in the specification this amino acid can
FT  also be Val"
FT  Modified-site 1452
FT  /note= "As given in the specification this amino acid can
FT  also be Tyr"
FT  Modified-site 1472
FT  /note= "As given in the specification this amino acid can
FT  also be Ser"
FT  Domain 1640..2000
FT  /label= NS4_domain
FT  Modified-site 1877
FT  /note= "As given in the specification this amino acid can
FT  also be Gly"
FT  Modified-site 1948
FT  /note= "As given in the specification this amino acid can
FT  also be His"
FT  Modified-site 1949
FT  /note= "As given in the specification this amino acid can
FT  also be Cys"
FT  Domain 2000..3011
FT  /label= NS5_domain
FT  Modified-site 2021
FT  /note= "As given in the specification this amino acid can
FT  also be Val"
FT  Modified-site 2348
FT  /note= "As given in the specification this amino acid can
FT  also be Ser"
FT  Modified-site 2385
FT  /note= "As given in the specification this amino acid can
FT  also be Phe"
FT  Modified-site 2386
FT  /note= "As given in the specification this amino acid can
FT  also be Ala"
FT  Modified-site 2502
FT  /note= "As given in the specification this amino acid can
FT  also be Phe"
FT  Modified-site 2690
FT  /note= "As given in the specification this amino acid can
FT  also be Gly"
FT  Modified-site 2921
FT  /note= "As given in the specification this amino acid can
FT  also be Gly"
FT  Modified-site 2996
FT  /note= "As given in the specification this amino acid can
FT  also be Pro"
FT
FT  US5712087-A.
XX
PN  27-JAN-1998.
XX
PD  12-MAY-1995; 95US-00440519.
XX
PR  04-APR-1990; 90US-00504352.
XX  07-JUL-1992; 92US-00910760.
XX
PA  (CHIR ) CHIRON CORP.
XX
PI  Kuo G, Houghton M, Choo Q;
XX
XX  WPI; 1998-119973/11.
XX  N-PSDB; AAV09989.
XX
PT  Immunoassays for hepatitis C virus antibodies - using combinations of
XX  antigenic fragments of HCV polyprotein.
XX
PS  Disclosure; Fig 1; 59pp; English.
XX
CC  This sequence represents the hepatitis C virus (HCV) polyprotein which is
```

CC used in the construction of novel combinations of HCV antigens that have
CC a broader range of immunological activity than any single HCV antigen. An
CC example of such an antigen given in this specification comprises a first
CC antigen containing at least 8 amino acids of the C domain of the HCV
CC polyprotein and a second antigen comprising at least 8 amino acids of the
CC NS3 domain, the NS4 domain, the S domain or the NS5 domain of the HCV
CC polyprotein in the form of a fusion protein, a physical mixture or bound
CC to a solid matrix. Note: The features given in the specification as
CC represented in the feature table of AAM40038 differ from the positions
CC indicated in Figure 1
XX
XX
SQ Sequence 3011 AA;

Query Match 99.5%; Score 3602; DB 2; Length 3011;
Best Local Similarity 99.6%; Pred. No. 4.3e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MAPITAYAAQQTGRLGCGIITSITGRDKNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
Db :|||||
Qy 61 GTRTIASPKGPVIQMYTNVDQDLVGPAPQSGRSITPTCTCGSSDLYLVTRHADVIPVRR 120
Db 1086 GTRTIASPKGPVIQMYTNVDQDLVGPAPQSGRSITPTCTCGSSDLYLVTRHADVIPVRR 1145
Qy 121 GDSRGSLLSPRPISVLKSGSGEPILCPAGHAGVGFRAAVCTRGVAKAVDFIPVENLETTM 180
Db 1146 GDSRGSLLSPRPISVLKSGSGEPILCPAGHAGVGFRAAVCTRGVAKAVDFIPVENLETTM 1205
Qy 181 RSPVFTDNSSPPVFPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLNPSVAATLGF 240
Db 1206 RSPVFTDNSSPPVFPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLNPSVAATLGF 1265
Qy 241 AYNSKAHGIDNIRTVRTITITGSPITYSTYTKFLADGCGSGAYDIIICDECHSTDATS 300
Db 1266 AYNSKAHGIDNIRTVRTITITGSPITYSTYTKFLADGCGSGAYDIIICDECHSTDATS 1325
Qy 301 ILGITVLDQAEATAGARLVLATATPPGVSVPVPHNIEEVALSTTGEIPFYGKAIPLEVI 360
Db 1326 ILGITVLDQAEATAGARLVLATATPPGVSVPVPHNIEEVALSTTGEIPFYGKAIPLEVI 1385
Qy 361 KGRHRLIFCHSKKKCKDELAALKVALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 420
Db 1386 KGRHRLIFCHSKKKCKDELAALKVALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 1445
Qy 421 GDFDSVIDCNVCTQTVDPSLDPTFTIITILPQDAVSRTQRRGRTGKPGIYRFVAPG 480
Db 1446 GDFDSVIDCNVCTQTVDPSLDPTFTIITILPQDAVSRTQRRGRTGKPGIYRFVAPG 1505
Qy 481 ERPSGMPDSSVLCYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWGVFTGL 540
Db 1506 ERPSGMPDSSVLCYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWGVFTGL 1565
Qy 541 THIDAHFLSQTKSGENLPYLVAQYATVCARAQAPPPSDQWKKLIRLKTPLHGPTPL 600
Db 1566 THIDAHFLSQTKSGENLPYLVAQYATVCARAQAPPPSDQWKKLIRLKTPLHGPTPL 1625
Qy 601 YELGAVQNEITLTHPVTKYIMTCHSADLEVVTSTWLVGGVLAALAAVCLSTGCVVIVGR 660
Db 1626 YELGAVQNEITLTHPVTKYIMTCHSADLEVVTSTWLVGGVLAALAAVCLSTGCVVIVGR 1685
Qy 661 VVLGSKPAIIPDREVLYREFDEMEBC 686
Db 1686 VVLGSKPAIIPDREVLYREFDEMEBC 1711

RESULT 14
AAE22049
ID AAE22049 standard; protein; 3011 AA.
XX
XX AAE22049;
AC AAE22049;
XX
XX 16-JUL-2002 (first entry)

XX Hepatitis C virus (HCV) polyprotein.
DE
XX
KW Hepatitis C virus; HCV; antigen; C domain; polyprotein; NS3 domain;
NS4 domain; S domain; NS5 domain.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT Domain 1..122
FT Domain /label= C_domain
FT Domain 199..328
FT Domain /label= S_domain
FT Region 1192..1931
FT Region /note= "c200 polypeptide"
FT Region 1192..1457 domain antigen"
FT Region /note= "NS3 domain antigen"
FT Region 1569..1931
FT Region /note= "NS4 antigen"
FT Region 2054..2464
FT Region /note= "NS5 antigen"
XX
XX US6312889-B1.
PN
XX
XX 06-NOV-2001.
XX
XX 12-MAY-1995; 95US-00440549.
XX
XX 04-APR-1990; 90US-00504352.
PR 07-JUL-1992; 92US-00910760.
XX
XX (CHIR) CHIRON CORP.
XX
XX Houghton M, Choo Q, Kuo G;
XX
XX WPI; 2002-040268/05.
DR N-PSDB; AAD35043.
XX
XX Combination of hepatitis C viral (HCV) antigens, useful in improved
immunoassay for detecting HCV antibodies.
XX
XX Example 1; Col 45-60; 58pp; English.
PS
XX
XX The invention relates to combination of hepatitis C viral (HCV) antigens
that have a broader range of immunological reactivity than any single HCV
antigen. The combinations consist of an antigen from the C domain of the
HCV polyprotein, and at least one additional HCV antigen from either the
NS3 domain, the NS4 domain, the S domain, or the NS5 domain and are in
the form of fusion protein, a simple physical mixture, or the individual
antigens commonly bound to a solid matrix. The combinations of antigens
provides broad range immunoassays for anti-HCV antibodies. The invention
therefore provides a method for detecting antibodies to HCV in a mammal
suspected of containing such antibodies. The present sequence is HCV
polyprotein. Note: This sequence SEQ.ID.NO:10 is stated to be similar to
the sequence shown in Fig 1 (AAE22052) of the specification. However
these sequences differ
XX
SQ Sequence 3011 AA;
Query Match 99.5%; Score 3602; DB 5; Length 3011;
Best Local Similarity 99.6%; Pred. No. 4.3e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MAPITAYAAQQTGRLGCGIITSITGRDKNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
Db 1026 LAPITAYAAQQTGRLGCGIITSITGRDKNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 1085
Qy 61 GTRTIASPKGPVIQMYTNVDQDLVGPAPQSGRSITPTCTCGSSDLYLVTRHADVIPVRR 120
Db 1086 GTRTIASPKGPVIQMYTNVDQDLVGPAPQSGRSITPTCTCGSSDLYLVTRHADVIPVRR 1145
Qy 121 GDSRGSLLSPRPISVLKSGSGEPILCPAGHAGVGFRAAVCTRGVAKAVDFIPVENLETTM 180
Db :|||||

Db 1146 GDSGSLSPRPISYLGSGGGPCLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 1205
QY 181 RSPVFTDSSPPVVPQSFQVAHLHPTGSGSKTKVPAAYAAQGYKVLVLMNPSVAATLGFG 240
Db 1206 RSPVFTDSSPPVVPQSFQVAHLHPTGSGSKTKVPAAYAAQGYKVLVLMNPSVAATLGFG 1265
QY 241 AYMSKAHGIDPNIRTCVTRITTTGSPITYSTYSGKFLADGGSGGAYDIIICDECHSDATS 300
Db 1266 AYMSKAHGIDPNIRTCVTRITTTGSPITYSTYSGKFLADGGSGGAYDIIICDECHSDATS 1325
QY 301 ILGIGTVLQDAETAGARLVVLAATATPPGSVTVVPHNIEEVALSTTGEIPIYKKAIPLEVI 360
Db 1326 ILGIGTVLQDAETAGARLVVLAATATPPGSVTVVPHNIEEVALSTTGEIPIYKKAIPLEVI 1385
QY 361 KGRHILFCHSKKKCDELAALVAGINAVAYYRGGLDVSVIPGIDVVVATDMLMTGYT 420
Db 1386 KGRHILFCHSKKKCDELAALVAGINAVAYYRGGLDVSVIPGIDVVVATDMLMTGYT 1445
QY 421 GPDFSVIDNCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGKPGIYRFVAPG 480
Db 1446 GPDFSVIDNCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGKPGIYRFVAPG 1505
QY 481 ERPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVQODHLEFWEGVFTGL 540
Db 1506 ERPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVQODHLEFWEGVFTGL 1565
QY 541 THIDAHFLSQTQSGENLPVLVAYQATVCARAQAPPPSWDMWKCLIRLKTPLHGTPLL 600
Db 1566 THIDAHFLSQTQSGENLPVLVAYQATVCARAQAPPPSWDMWKCLIRLKTPLHGTPLL 1625
QY 601 YRLGAVQNEITLTHPVTKYIMTCSADLEVVTSWVLVGVLAALAAAYCLSTGCVVIVGR 660
Db 1626 YRLGAVQNEITLTHPVTKYIMTCSADLEVVTSWVLVGVLAALAAAYCLSTGCVVIVGR 1685
QY 661 VVLSGKPAIIPDREVLRYRFDMEEC 686
Db 1686 VVLSGKPAIIPDREVLRYRFDMEEC 1711

RESULT 15

AAE18688

ID AAE18688 standard; protein; 728 AA.

XX AC AAE18688;

XX DT 17-MAY-2002 (first entry)

XX DE NS3/4a mutant conformational antigen.

XX KW Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; mutein.

XX OS Unidentified.

XX FH Key

XX FT Misc-difference 182

XX FT /note= "wild type Ser is substituted with Ala"

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

XX FT

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XX FT

XX FT

XX FT

XX FT

XX Immunoassay solid support useful for detecting hepatitis C virus
PT infection in a biological sample, comprises at least one of HCV anti-core
PT antibody and HCV NS3/4a epitope, bound to the support.

XX Disclosure; Fig 3; 87pp; English.

XX The present invention relates to hepatitis C virus (HCV) core antigen and
CC NS (nonstructural) 3/4a antibody combination assay that can detect both
CC HCV antigens and antibodies present in a sample using a single solid
CC matrix as well as immunoassay solid supports for use in the assay. The
CC solid support is useful for detecting HCV infection in a biological
CC sample. The present sequence is NS3/4a mutant conformational antigen.
CC This sequence is used in the exemplification of the invention

XX Sequence 728 AA;

Query Match 99.5%; Score 3600; DB 5; Length 728;

Best Local Similarity 99.8%; Pred. No. 7.9e-305;

Matches 682; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 APITAYAAQOTRGLGCIITSLTGRDNQVEGEVQIVSTAAQTFLATCINGVCWTVVHGAG 61

Db 44 APITAYAAQOTRGLGCIITSLTGRDNQVEGEVQIVSTAAQTFLATCINGVCWTVVHGAG 103

QY 62 TRTIASPKGPVIQMYTNVDQDLVGFPAQGSRLTPTCTGSSDLVLTTRHADVIPVRRRG 121

Db 104 TRTIASPKGPVIQMYTNVDQDLVGFPAQGSRLTPTCTGSSDLVLTTRHADVIPVRRRG 163

QY 122 DSRGSLSPRPISYLGSGGGPCLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTMR 181

Db 164 DSRGSLSPRPISYLGSGGGPCLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTMR 223

QY 182 SPVFTDNSSPPVVPQSFQVAHLHPTGSGSKTKVPAAYAAQGYKVLVLMNPSVAATLGFGA 241

Db 224 SPVFTDNSSPPVVPQSFQVAHLHPTGSGSKTKVPAAYAAQGYKVLVLMNPSVAATLGFGA 283

QY 242 YMSKAHGIDPNIRTCVTRITTTGSPITYSTYSGKFLADGGSGGAYDIIICDECHSDATS 301

Db 284 YMSKAHGIDPNIRTCVTRITTTGSPITYSTYSGKFLADGGSGGAYDIIICDECHSDATS 343

QY 302 LGIGTVLQDAETAGARLVVLAATATPPGSVTVVPHNIEEVALSTTGEIPIYKKAIPLEVIK 361

Db 344 LGIGTVLQDAETAGARLVVLAATATPPGSVTVVPHNIEEVALSTTGEIPIYKKAIPLEVIK 403

QY 362 GGRHILFCHSKKKCDELAALVAGINAVAYYRGGLDVSVIPGIDVVVATDMLMTGYTG 421

Db 404 GGRHILFCHSKKKCDELAALVAGINAVAYYRGGLDVSVIPGIDVVVATDMLMTGYTG 463

QY 422 DFDSVIDNCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGKPGIYRFVAPGE 481

Db 464 DFDSVIDNCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGKPGIYRFVAPGE 523

QY 482 RPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVQODHLEFWEGVFTGLT 541

Db 524 RPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVQODHLEFWEGVFTGLT 583

QY 542 HIDAHLFSLQTKSGENLPVLVAYQATVCARAQAPPPSWDMWKCLIRLKTPLHGTPLL 601

Db 584 HIDAHLFSLQTKSGENLPVLVAYQATVCARAQAPPPSWDMWKCLIRLKTPLHGTPLL 643

QY 602 RLGAQVONEITLTHPVTKYIMTCSADLEVVTSWVLVGVLAALAAAYCLSTGCVVIVGRV 661

Db 644 RLGAQVONEITLTHPVTKYIMTCSADLEVVTSWVLVGVLAALAAAYCLSTGCVVIVGRV 703

QY 662 VVLSGKPAIIPDREVLRYRFDMEEC 686

Db 704 VVLSGKPAIIPDREVLRYRFDMEEC 728

Search completed: June 21, 2004, 10:30:03

Job time : 44.9396 secs

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